



(12) EUROPEAN PATENT APPLICATION

(43) Date of publication:
09.09.1998 Bulletin 1998/37

(21) Application number: 98104783.0

(22) Date of filing: 30.07.1993

(51) Int. Cl.⁵: C12N 15/62, C12N 15/31,
C12N 15/54, C12N 1/21,
C07K 14/33, C07K 14/435,
A61K 39/08

(84) Designated Contracting States:
AT BE CH DE DK ES FR GB GR IE IT LI LU MC NL
PT SE

(30) Priority: 31.07.1992 GB 9216317
26.03.1993 GB 9306398

(62) Document number(s) of the earlier application(s) in
accordance with Art. 76 EPC:
93917957.8 / 0 652 962

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Remarks:

This application was filed on 16 - 03 - 1998 as a
divisional application to the application mentioned
under INID code 62.

(54) Expression of recombinant fusion proteins in attenuated bacteria

(57) A fusion protein which is a tetanus toxin frag-
ment C linked at its C-terminal to a heterologous second
protein.

Description

This invention relates to DNA constructs, replicable expression vectors containing the constructs, attenuated bacteria containing the constructs and vaccines containing the said bacteria.

5 In recent years, there has emerged a new generation of live oral salmonella vaccines based upon strains of Salmonella which have been attenuated by the introduction of a non-reverting mutation in a gene in the aromatic biosynthetic pathway of the bacterium. Such strains are disclosed, for example, in EP-A-0322237. The aforesaid live oral salmonella vaccines are showing promise as vaccines for salmonellosis in man and animals, and they can also be used effectively as carriers for the delivery of heterologous antigens to the immune system. Combined salmonella vaccines have been
10 used to deliver antigens from viruses, bacteria, and parasites, eliciting secretory, humoral and cell-mediated immune responses to the recombinant antigens. Combined salmonella vaccines show great potential as single dose oral multi-vaccine delivery systems [C. Hormaeche *et al*, FEMS Symposium No. 63, Plenum, New York; pp 71-83, 1992].

There are problems to be overcome in the development of combined salmonella vaccines. A major consideration is obtaining a high level of expression of the recombinant antigen in the salmonella vaccine so that it will be sufficient
15 to trigger an immune response. However, unregulated high level expression of foreign antigens can be toxic and affect cell viability [I. Charles and G. Dougan, TIBTECH 8, pp 117-21, 1990], rendering the vaccine ineffective or causing loss of the recombinant DNA. Several possible solutions to this problem have been described, such as expression from plasmids carrying essential genes, "on-off" promoters or incorporation of the foreign genes into the salmonella chromosome.

20 An alternative approach to overcoming the aforesaid problem would be to use a promoter which is inducible *in vivo*, and one such promoter is the E.coli nitrite reductase promoter nirB which is induced under anaerobiosis and has been used in biotechnology for the production of tetanus toxin fragment C (TetC) of Clostridium tetani [M.D. Oxer *et al* Nud. Ac. Res., 19, pp 2889-92, 1991]. It has previously been found by the inventors of this application (S.N. Chatfield *et al* Bio/Technology, Vol. 10, pp 888-92 1992) that an Aro Salmonella harbouring a construct expressing TetC from the nirB
25 promoter (pTETnir15) elicited very high anti-tetanus antibody responses in mice. The article by Chatfield *et al* was published after the priority date of this application.

However, we have also found that when it was attempted to express the P28 antigen from Schistosoma mansoni alone from nirB, the resulting construct was not immunogenic.

Tetanus toxoid has been extensively used as an adjuvant for chemically coupled guest epitopes [D.A. Herrington *et al* Nature, 328, pp 257-9 1987]. The potent immunogenicity of TetC in Salmonella suggested to us that it may be possible to exploit this character to promote the immune response of the guest peptides or proteins. However, fusing two proteins together often leads to an incorrectly folded chimaeric protein which no longer retains the properties of the individual components. For example the B subunit of the Vibrio cholerae (CT-B) and E.coli (LT-B) enterotoxins are powerful mucosal immunogens but genetic fusions to these subunits can alter the structure and properties of the carrier and
35 hence their immunogenicity [see M. Sandkvist *et al*, J. Bacteriol 169, pp 4570-6, 1987, Clements 1990 and M. Lipscombe *et al* [Mol. Microbiol 5, pp 1385 1990]. Moreover, many heterologous genes expressed in bacteria are not produced in soluble properly folded, or active forms and tend to accumulate as insoluble aggregates [see C. Schein *et al*, Bio/Technology 6, pp 291-4, 1988 and R. Halenbeck *et al*, Bio/Technology 7, pp 710-5, 1989].

It is an object of the invention to overcome the aforementioned problems.

40 We have now found that efficient expression of recombinant antigens, and in particular fusion proteins, can be achieved in bacteria such as salmonellae, by the use of an inducible promoter such as nirB and by incorporating a flexible hinge region between two antigenic components of the fusion protein. The resulting recombinant antigens have been shown to have good immunogenicity. It has also been found, surprisingly, that enhanced expression of a protein can be obtained when a gene coding for the protein is linked to the gene for tetanus toxin C fragment.

45 Accordingly, in a first aspect, the present invention provides a DNA construct comprising a promoter sequence operably linked to a DNA sequence encoding first and second proteins linked by a hinge region, characterised in that the promoter sequence is one having activity which is induced in response to a change in the surrounding environment.

In another aspect, the invention provides a DNA construct comprising a promoter sequence operably linked to a DNA sequence encoding linked first and second proteins, wherein the first heterologous protein is an antigenic

transforming an attenuated bacterium with a DNA construct as hereinbefore defined.

The invention also provides a vaccine composition comprising an attenuated bacterium, or a fusion protein, as hereinbefore defined, and a pharmaceutically acceptable carrier.

The first and second proteins are preferably heterologous proteins and in particular can be polypeptide immunogens; for example they may be antigenic sequences derived from a virus, bacterium, fungus, yeast or parasite. In particular, it is preferred that the first said protein is an antigenic sequence comprising tetanus toxin fragment C or epitopes thereof.

The second protein is preferably an antigenic determinant of a pathogenic organism. For example, the antigenic determinant may be an antigenic sequence derived from a virus, bacterium, fungus, yeast or parasite.

Examples of viral antigenic sequences for the first and/or second heterologous proteins are sequences derived from a type of human immuno-deficiency virus (HIV) such as HIV-1 or HIV-2, the CD4 receptor binding site from HIV, for example from HIV-1 or -2, hepatitis A or B virus, human rhinovirus such as type 2 or 14, Herpes simplex virus, poliovirus type 2 or 3, foot-and-mouth disease virus (FMDV), rabies virus, rotavirus, influenza virus, coxsackie virus, human papilloma virus (HPV), for example the type 16 papilloma virus, the E7 protein thereof, and fragments containing the E7 protein or its epitopes; and simian immunodeficiency virus (SIV). Examples of antigens derived from bacteria are those derived from *Bordetella pertussis* (e.g. P69 protein and filamentous haemagglutinin (FHA) antigens), *Vibrio cholerae*, *Bacillus anthracis*, and *E.coli* antigens such as *E.coli* heat labile toxin B subunit (LT-B), *E.coli* K88 antigens, and enterotoxigenic *E.coli* antigens. Other examples of antigens include the cell surface antigen CD4, *Schistosoma mansoni* P28 glutathione S-transferase antigens (P28 antigens) and antigens of flukes, mycoplasma, roundworms, tapeworms, *Chlamydia trachomatis*, and malaria parasites, eg. parasites of the genus plasmodium or babesia, for example *Plasmodium falciparum*, and peptides encoding immunogenic epitopes from the aforementioned antigens.

Particular antigens include the full length *Schistosoma mansoni* P28, and oligomers (e.g. 2, 4 and 8-mers) of the immunogenic P28 aa 115-131 peptide (which contains both a B and T cell epitope), and human papilloma virus E7 protein, Herpes simplex antigens, foot and mouth disease virus antigens and simian immunodeficiency virus antigens.

The promoter sequence is one having activity which is induced in response to a change in the surrounding environment, and an example of such a promoter sequence is one which has activity which is induced by anaerobic conditions. A particular example of such a promoter sequence is the *nirB* promoter which has been described, for example in International Patent Application PCT/GB92/00387. The *nirB* promoter has been isolated from *E.coli*, where it directs expression of an operon which includes the nitrite reductase gene *nirB* (Jayaraman *et al*, J. Mol. Biol. **196**, 781-788, 1987), and *nirD*, *nirC*, *cysG* (Peakman *et al*, Eur. J. Biochem. **191**, 315-323, 1990). It is regulated both by nitrite and by changes in the oxygen tension of the environment, becoming active when deprived of oxygen, (Cole, Biochem. Biophys. Acta. **162**, 356-368, 1968). Response to anaerobiosis is mediated through the protein FNR, acting as a transcriptional activator, in a mechanism common to many anaerobic respiratory genes.

By deletion and mutational analysis the part of the promoter which responds solely to anaerobiosis has been isolated and by comparison with other anaerobically-regulated promoters a consensus FNR-binding site has been identified (Bell *et al*, Nucl. Acids. Res. **17**, 3865-3874, 1989; Jayaraman *et al*, Nucl. Acids. Res. **17**, 135-145, 1989). It has also been shown that the distance between the putative FNR-binding site and the -10 homology region is critical (Bell *et al*, Molec. Microbiol. **4**, 1753-1763, 1990). It is therefore preferred to use only that part of the *nirB* promoter which responds solely to anaerobiosis. As used herein, references to the *nirB* promoter refer to the promoter itself or a part or derivative thereof which is capable of promoting expression of a coding sequence under anaerobic conditions. The preferred sequence, and which contains the *nirB* promoter is:

AATTCAGGTAAATTTGATGTACATCAAATGGTACCCCTTGCTGAATCGTTAAGG

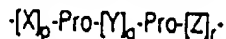
TAGGCGGTAGGGCC (SEQ ID NO: 1)

The hinge region is a region designed to promote the independent folding of both the first and second proteins by providing both spatial and temporal separation between the domains.

The hinge region typically is a sequence encoding a high proportion of proline and/or glycine amino acids. The

Without wishing to be bound by any theory, the prolines are thought to form the rigid part of the hinge as the ring structure characteristic of this amino acid hinders rotation around the peptide bond that connects the proline residue with an adjacent amino acid. This property is thought to prevent proline, and adjacent residues, from adopting the ordered structure of an alpha helix or beta strand. Flexibility is thought to be imparted by glycine, the simplest amino acid, with very limited steric demands. Glycine is thought to function as a flexible elbow in the hinge. Other amino acids may be substituted for glycine, particularly those without bulky side-chains, such as alanine, serine, asparagine and threonine.

In one preferred embodiment, the hinge region is a chain of four or more amino acids defining the sequence



wherein Pro is proline, X and Y are each glycine, or an amino acid having a non-bulky side chain; Z is any amino acid; p is a positive integer; q is a positive integer of from one to ten; and r is zero or a positive integer greater than zero.

The hinge region can be a discrete region heterologous to both the first and second proteins or can be defined by a carboxy-end portion of the first protein or an amino-end portion of the second protein.

Codons which are infrequently utilized in *E. coli* [H. Grosjean *et al.*, Gene 18, 199-209, 1982] and *Salmonella* are selected to encode for the hinge, as such rare codons are thought to cause ribosomal pausing during translation of the messenger RNA and allow for the correct folding of polypeptide domains [I.J. Purvis *et al.*, J. Mol. Biol. 193, 413-7 1987]. In addition, where possible restriction enzymes are chosen for the cloning region which, when translated in the resulting fusion, do not encode for bulky or charged side-groups.

In a most preferred aspect, the present invention provides a DNA molecule comprising the *nirB* promoter operably linked to a DNA sequence encoding first and second polypeptide immunogens linked by a hinge region, wherein the first polypeptide immunogen comprises tetanus toxin fragment C or epitopes thereof.

Also disclosed is a DNA construct comprising a promoter sequence whose activity is induced in response to a change in the surrounding environment, said promoter sequence being operably linked to a DNA sequence encoding a first antigenic sequence and a hinge region, and at or adjacent the 3'-end thereof one or more restriction sites for the introduction of a second antigenic sequence.

Further disclosure includes a DNA construct comprising a promoter sequence operably linked to a first DNA sequence encoding Tetanus toxin C fragment, or one or more epitopes thereof, and a hinge region which has at or adjacent to the 3'-end thereof one or more restriction sites for the introduction of a second antigenic sequence. The promoter of such a DNA construct may have an activity which is induced in response to a change in the surrounding environment. Thus, the activity of the promoter may be induced by anaerobic conditions. Such a promoter may be the *nirB* promoter or a part or derivative thereof which is capable of promoting expression of a sequence under anaerobic condition.

In another preferred aspect of the invention, there is provided a replicable expression vector, suitable for use in bacteria, containing the *nirB* promoter sequence operably linked to a DNA sequence encoding first and second polypeptide immunogens linked by a hinge region, wherein the first polypeptide immunogen comprises tetanus toxin fragment C or epitopes thereof.

It has been found that by providing a DNA sequence encoding tetanus fragment C (TetC) linked via a hinge region to a second sequence encoding an antigen, the expression of the sequence in bacterial cells is enhanced relative to constructs wherein the fragment C and hinge region are absent. For example, the expression level of the full length P28 protein of *S. mansoni* when expressed as a fusion to TetC was greater than when the P28 protein was expressed alone from the *nirB* promoter. The TetC fusions to the full length P28 protein of *S. mansoni* and its tandem epitopes were all soluble and expressed in both *E. coli* and *S. typhimurium*. In addition, the TetC-P28 fusion protein was capable of being affinity purified by a glutathione agarose matrix, suggesting that the P28 had folded correctly to adopt a conformation still capable of binding to its natural substrate.

Stable expression of the first and second heterologous proteins linked by the hinge region can be obtained *in vivo*. The heterologous proteins can be expressed in an attenuated bacterium which can thus be used as a vaccine.

The attenuated bacterium may be selected from the genera *Salmonella*, *Bordetella*, *Vibrio*, *Haemophilus*, *Neisseria* and *Yersinia*. Alternatively, the attenuated bacterium may be an attenuated strain of enterotoxigenic *Escherichia coli*. In particular the following species can be mentioned: *S. typhi* - the cause of human typhoid; *S. typhimurium* - the cause of salmonellosis in several animal species; *S. enteritidis* - a cause of food poisoning in humans; *S. choleraesuis* - a cause of salmonellosis in pigs; *Bordetella pertussis* - the cause of whooping cough; *Haemophilus influenzae* - a cause of meningitis; *Neisseria gonorrhoeae* - the cause of gonorrhoea; and *Yersinia* - a cause of food poisoning.

Preferably, however, an attenuated bacterium harbours a non-reverting mutation in each of two discrete genes in its aromatic amino acid biosynthetic pathway. Such bacteria are disclosed in EP-A-0322237. Double *aro* mutants which are suitable are *aroA aroC*, *aroA aroD*, and *aroA aroE*. Other bacteria having mutations in other combinations of the *aroA*, *aroC*, *aroD* and *aroE* genes are however useful. Particularly preferred are *Salmonella* double *aro* mutants, for example double *aro* mutants of *S.typhi* or *S.typhimurium*, in particular *aroA aroC*, *aroA aroD* and *aroA aroE* mutants. Alternatively, the attenuated bacterium may harbour a non-reverting mutation in a gene concerned with the regulation of one or more other genes (EP-A-0400958). Preferably the mutation occurs in the *ompR* gene or another gene involved in regulation. There are a large number of other genes which are concerned with regulation and are known to respond to environmental stimuli (Ronson *et al*, Cell 49, 579-581).

This type of attenuated bacterium may harbour a second mutation in a second gene. Preferably the second gene is a gene encoding for an enzyme involved in an essential biosynthetic pathway, in particular genes involved in the pre-chorismate pathway involved in the biosynthesis of aromatic compounds. The second mutation is therefore preferably in the *aroA*, *aroC* or *aroD* gene.

Another type of attenuated bacterium is one in which attenuation is brought about by the presence of a non-reverting mutation in DNA of the bacterium which encodes, or which regulates the expression of DNA encoding, a protein that is produced in response to environmental stress. Such bacteria are disclosed in WO 91/15572. The non-reverting mutation may be a deletion, insertion, inversion or substitution. A deletion mutation may be generated using a transposon.

An attenuated bacterium containing a DNA construct according to the invention can be used as a vaccine. Fusion proteins (preferably in substantially pure form) expressed by the bacteria can also be used in the preparation of vaccines. For example, a purified TetC-P28 fusion protein has been found to be immunogenic on its own. In a further aspect therefore, the invention provides a vaccine composition comprising a pharmaceutically acceptable carrier or diluent and, as active ingredient, an attenuated bacterium or fusion protein as hereinbefore defined.

The vaccine may comprise one or more suitable adjuvants.

The vaccine is advantageously presented in a lyophilised form, for example in a capsular form, for oral administration to a patient. Such capsules may be provided with an enteric coating comprising, for example, Eudragit "S", Eudragit "L", Cellulose acetate, Cellulose acetate phthalate or Hydroxypropylmethyl Cellulose. These capsules may be used as such, or alternatively, the lyophilised material may be reconstituted prior to administration, e.g. as a suspension. Reconstitution is advantageously effected in buffer at a suitable pH to ensure the viability of the organisms. In order to protect the attenuated bacteria and the vaccine from gastric acidity, a sodium bicarbonate preparation is advantageously administered before each administration of the vaccine. Alternatively, the vaccine may be prepared for parenteral administration, intranasal administration or intramammary administration.

The attenuated bacterium containing the DNA construct of the invention may be used in the prophylactic treatment of a host, particularly a human host but also possibly an animal host. An infection caused by a micro-organism, especially a pathogen, may therefore be prevented by administering an effective dose of an attenuated bacterium according to the invention. The bacterium then expresses a heterologous protein or proteins capable of raising antibody to the micro-organism. The dosage employed will be dependent on various factors including the size and weight of the host, the type of vaccine formulated and the nature of the heterologous protein.

An attenuated bacterium according to the present invention may be prepared by transforming an attenuated bacterium with a DNA construct as hereinbefore defined. Any suitable transformation technique may be employed, such as electroporation. In this way, an attenuated bacterium capable of expressing a protein or proteins heterologous to the bacterium may be obtained. A culture of the attenuated bacterium may be grown under aerobic conditions. A sufficient amount of the bacterium is thus prepared for formulation as a vaccine, with minimal expression of the heterologous protein occurring.

The DNA construct may be a replicable expression vector comprising the *nirB* promoter operably linked to a DNA sequence encoding the tetanus toxin C fragment or epitopes thereof and the second heterologous protein, linked by a hinge region. The *nirB* promoter may be inserted in an expression vector, which already incorporates a gene encoding one of the heterologous proteins (e.g. tetanus toxin C fragment), in place of the existing promoter controlling expression of the protein. The hinge region and gene encoding the second heterologous protein (e.g. an antigenic sequence) may then be inserted. The expression vector should, of course, be compatible with the attenuated bacterium into which the vector is to be inserted.

The expression vector is provided with appropriate transcriptional and translational control elements.

aspect of the invention.

Figure 2 is a schematic illustration of the construction of a second intermediate plasmid pTECH2.

Figure 3 is a schematic illustration of the construction of a plasmid of the invention using the intermediate plasmid of Figure 2 as the starting material. In Figure 3 B = BamHI, E = EcoRV; H = HindIII; X = XbaI; S = SpeI.

Figure 4 is a schematic illustration of the construction of a plasmid containing repeating epitopes (reptopes).

Figure 5 illustrates antibody responses against recombinant *S. mansoni* protein P28 as detected by ELISA in mice inoculated intravenously with SL3261, SL3261(pTETnir15), SL3261 (pTECH2), SL3261(pTECH2-monomer), SL3261 (pTECH2-dimer), SL3261(pTECH2-tetramer), SL3261(pTECH2-octamer), and SL3261(pTECH1-P28). In Figure 5 the results are expressed as OD in individual mice at intervals after immunisation.

Figure 6 illustrates antibody responses against TetC as detected by ELISA in mice inoculated as in Figure 5.

Figure 7 illustrates antibody responses against peptide 115-131 of the P28 protein coupled to ovalbumin as detected by ELISA in mice inoculated intravenously with SL3261, SL3261(pTECH2), SL3261(pTECH2-monomer), SL3261(pTECH2-dimer), SL3261(pTECH2-tetramer), and SL3261(pTECH2-octamer).

Figure 8 illustrates antibody responses against TetC as detected by ELISA from mice inoculated orally with SL3261(pTECH1-P28).

Figure 9 illustrates antibody responses against recombinant P28 as detected by ELISA in mice inoculated as in Figure 8.

Figure 10 illustrates schematically the preparation of various constructs from the pTECH2 intermediate plasmid.

Figure 11 illustrates schematically the structure of tripartite protein structures ("heteromers") prepared using pTECH2.

Figure 12 shows the DNA sequence of the vector pTECH1. (SEQ ID NO: 17).

Figure 13 shows the DNA sequence of the vector pTECH2. (SEQ ID NO: 18).

Figure 14 illustrates, schematically, the restriction sites on the vector pTECH2.

EXAMPLE 1

Preparation of pTECH1

The preparation of pTECH1, a plasmid incorporating the *nirB* promoter and TetC gene, and a DNA sequence encoding a hinge region and containing restriction endonuclease sites to allow insertion of a gene coding for a second or guest protein, is illustrated in Figure 1. Expression plasmid pTETnir15, the starting material shown in Figure 1, was constructed from pTETlac115 (Makoff *et al*, Nucl. Acids Res. 17 10191-10202, 1989); by replacing the EcoRI-ApaI region (1354bp) containing the lacI gene and lac promoter with the following pair of oligos 1 and 2:

Oligo-1 5' AATTCAGGTAAATTTGATGTACATCAAATGGTACCCCTTGCTGAAT

Oligo-2 3' -GTCCATTTAAACTACATGTAGTTTACCATGGGGAACGACTTA

CGTTAAGGTAGGCGGTAGGGCC-3' (SEQ ID NO: 2)

GCAATTCCATCCGCCATC-5' (SEQ ID NO: 3)

The oligonucleotides were synthesised on a Pharmacia Gene Assembler and the resulting plasmids confirmed by sequencing (Makoff *et al*, Bio/Technology 7, 1043-1046, 1989).

The pTETnir15 plasmid was then used for construction of the novel pTECH1 plasmid incorporating a polylinker region suitable as a site for insertion of heterologous DNA to direct the expression of fragment C fusion proteins. pTETnir15 is a known pAT153-based plasmid which directs the expression of fragment C. However, there are no naturally occurring convenient restriction sites present at the 3'-end of the TetC gene. Therefore, target sites, preceded by a hinge region, were introduced at the 3'-end of the TetC coding region by means of primers tailored with "add-on" adapter sequences (Table 1), using the polymerase chain reaction (PCR) [K. Mullis *et al*, Cold Spring Harbor Sym. Quant. Biol. 51, 263-273 1986]. Accordingly, pTETnir15 was used as a template in a PCR reaction using primers corresponding to regions covering the SacII and BamHI sites. The anti-sense primer in this amplification was tailored with a 38 base 5'-adaptor sequence. The anti-sense primer was designed so that a sequence encoding novel XbaI, SpeI and BamHI sites were incorporated into the PCR product. In addition, DNA sequences encoding additional extra amino

The PCR product was gel-purified and digested with SacII and BamHI, and cloned into the residual 2.8 kb vector pTETnir15 which had previously been digested by SacII and BamHI. The resulting plasmid purified from transformed colonies and named pTECH 1 is shown in Figure 1. Heterologous sequences such as the sequence encoding the Schistosoma mansoni P28 glutathione S-transferase (P28) were cloned into the XbaI SpeI and BamHI sites in accordance with known methods.

EXAMPLE 2

Construction of pTECH2

To further improve the utility of pTECH1, a short linker sequence was introduced between the XbaI and BamHI sites in pTECH1 to allow the directional cloning of oligonucleotides and to also facilitate the construction of multiple tandem epitopes, ("repitopes") (Figure 2). Two complementary oligonucleotides were synthesized bearing the restriction enzyme target sites for BamHI, EcoRV, HindIII, SpeI, followed by a translational stop codon (Table 1). The oligonucleotides were tailored with XbaI and BamHI cohesive ends; however, the BamHI target sequence was designed to include a mismatch and, upon cloning, this restriction site in pTECH1 is destroyed. This version of the vector was designated pTECH2.

EXAMPLE 3

Construction of pTECH1-P28

A P28 gene expression cassette was produced by PCR using pUC19-P28 DNA (a kind gift from Dr R Pierce, Pasteur Institute, Lille) as template. Oligonucleotide primers were designed to amplify the full length P28 gene beginning with the start codon and terminating with the stop codon. In addition, the sense and antisense primers were tailored with the restriction sites for XbaI and BamHI respectively. The product was gel-purified and digested with XbaI and BamHI and then cloned into pTECH1 which had previously been digested with these enzymes and subsequently gel-purified.

Expression of the TetC-P28 fusion protein

Expression of the TetC-P28 fusion protein was evaluated by SDS-PAGE and Western blotting of bacterial cells harbouring the construct. It was found that the fusion protein remains soluble, cross-reacts with antisera to both TetC and P28, and is also of the expected molecular weight, 80kDa, for a full length fusion.

The fusion protein was stably expressed in a number of different genetic backgrounds including E. coli (TG2) and S. typhimurium (SL5338, SL3261) as judged by SDS-PAGE and Western blotting. Of interest was a minor band of 50kDa which co-migrates with the TetC-Hinge protein alone and cross-reacts exclusively with the anti-TetC sera is visible in a Western blot. As the codon selection in the hinge region has been designed to be suboptimal, the rare codons may cause pauses during translation which may occasionally lead to the premature termination of translation, thus accounting for this band.

Affinity purification of the TetC-P28 fusion

Glutathione is the natural substrate for P28, a glutathione S-transferase. The amino acid residues involved in binding glutathione are thought to be spatially separated in the primary structure of the polypeptide and brought together to form a glutathione binding pocket in the tertiary structure (P. Reinemer *et al.* EMBO, J8, 1997-2005, 1991). In order to gauge whether the P28 component of the fusion has folded correctly to adopt a conformation capable of binding glutathione, its ability to be affinity purified on a glutathione-agarose matrix was tested. The results obtained (not shown) demonstrated that the TetC-P28 fusion protein binds to the glutathione-agarose matrix and is eluted with free glutathione.

SpeI (Figure 3).

Repeated tandem copies of the epitopes (repeptides) were constructed in pTECH2 by the following approach. The recombinant fusion vector was digested with XbaI and SpeI and to each digest was added a second restriction enzyme which cuts uniquely elsewhere within the vector, e.g. PstI which makes a cut exclusively within the ampicillin resistance gene (Figure 4). DNA fragments containing the epitope sequences can be purified from each of the double digests, mixed and then ligated. XbaI cleaves its target sequence to generate a 5'-CTAG overhang which is compatible with the SpeI overhang. Upon ligation the recognition sequences of both these enzymes are destroyed. In this way the XbaI-SpeI restriction sites remain unique and the procedure can be simply and effectively repeated to construct recombinant fusion vectors expressing four or eight tandem copies of the epitopes (Figure 4). A similar strategy has been used by others in the generation of a multimeric fusion protein for the production of a neuropeptide [T. Kempe *et al.* Gene 39, 239-45, 1985].

Expression of the TetC-peptide fusion proteins

Expression of the TetC-peptide fusions as monomeric, dimeric, tetrameric, and octameric tandem peptide repeats was evaluated by SDS-PAGE and Western blotting of the bacterial strains harbouring the constructs. The fusion proteins remain soluble, cross-react with both antisera to TetC and P28, and are also of the expected molecular weight (Figure 5). Furthermore the fusion proteins are expressed in a number of different genetic backgrounds including E. coli (TG2) and S. typhimurium (SL5338, SL3261) as judged by SDS-PAGE and Western blotting. There appeared to be some degradation of the peptides consisting of higher numbers of copies, as indicated by the appearance of faint bands of lower molecular weight seen in Western blots probed with the anti-P28 antibody. The size of the bands suggested that they consisted of reduced copy number fusions to TetC. As was the case with the TetC-P28 fusion described above, the level of expression of the TetC-peptide fusions was less than that of TetC alone from pTECH2, with the expression level gradually decreasing with increasing copy number.

EXAMPLE 5

Immunological Studies

Stability of the plasmid constructs in vivo and immunization of mice

BALB/c mice were given approx. 10^6 cfu i/v or 5×10^9 orally of S. typhimurium SL3261 and SL3261 harbouring the different constructs. Viable counts on homogenates of liver, spleen and (for orally inoculated mice) lymph nodes performed from days 1-8 (epitope fusions) and 1-11 (vector, octamer and P28 fusions) were similar on media with and without ampicillin, indicating that the plasmids were not being lost during growth in the tissues.

Antibody responses in mice immunized intravenously

Antibody responses to the TetC-P28 fusion

Tail bleeds were taken weekly on weeks 3 to 6 from animals from each group of 8 mice. Figure 5 shows that in mice immunized with salmonellae expressing the TetC-P28 fusion, antibody responses to recombinant P28 appeared by week 3, and were positive in 6/6 mice from week 4 onwards. No anti-P28 antibodies were detected in sera from mice immunised with either SL3261 or SL3261-pTETnir15 or pTECH2.

All mice immunized with salmonellae expressing TetC, either alone or as the TetC-P28 fusion (but not with salmonellae alone), made antibody to TetC appearing as early as the third week (Figure 6).

Thereafter sera from at least two mice injected with the octameric fusion consistently recognized P28 from week four up to week six.

In summary the antibody responses against the epitopes improved dramatically with increasing copy number, with the tetrameric and octameric epitope fusions being the most potent. No antibody responses to the monomeric fusion were detected.

Antibody response to TetC in mice immunised with the different fusions

The antibody response to TetC was not the same in all groups; the addition of C-terminal fusions to TetC clearly modified the response. Figure 6 shows that the antibody response to TetC elicited by the vector pTECH2 (TetC-Hinge alone) was significantly less than the TetC response to the parental vector, pTETnir15. Surprisingly, the addition to TetC of fusions of increasing size dramatically restores the response to TetC. The anti-TetC response to the largest fusion, full length P28 in pTECH1, was similar to the response to TetC obtained from the parental plasmid (under the conditions tested). Sera from mice injected with non-recombinant SL3261 did not react with TetC at any time during the period tested.

Antibody responses in mice immunized orally

Groups of 10 mice were immunized orally with approx. 5×10^9 cfu of SL3261 alone or carrying pTECH1, or pTECH1-P28, given intragastrically in 0.2ml via a gavage tube. Bleeds taken from week 3 to week 10 showed that most mice receiving the recombinant salmonellae made antibody to TetC as early as week 3 (Figure 8). Mice immunised with the TetC-P28 fusion made antibody to P28 which was detectable in approximately half of the mice by week 8, and then declined (Figure 9).

Antibody responses in mice immunized with the purified fusion protein

Mice were immunized subcutaneously with affinity purified TetC-P28 fusion protein adsorbed on aluminium hydroxide. Controls received commercial tetanus toxoid alone. Preliminary results indicate that animals given the fusion protein make an antibody response to both TetC and to P28 (data not shown). No anti-P28 antibody was detected in mice given tetanus toxoid.

T-cell responses to TetC and P28

Mice were immunized i/v with approximately 10^6 cfu of SL3261, SL3261(pTETnir15) and SL3261(pTECH1-P28). Six months later T-cell responses as IL-2/IL-4 production were measured against salmonella whole cell soluble extract, TetC, recombinant P28 and whole adult worm antigen as described in the section headed Materials and Methods below. Table 2 shows that cells from both groups produced an IL-2/IL-4 response to the sodium hydroxide treated salmonella extract and to TetC. However, cells from mice immunized with the salmonellae expressing the TetC-P28 fusion also responded to both recombinant P28 and whole worm extract.

Thus the salmonella delivery system has elicited both humoral and cellular (T-cell) immune responses to P28.

The salmonellae expressing the recombinant antigens all persisted in the mouse tissues as well as the parental strain, and the plasmids were not lost *in vivo*.

Constructs expressing higher molecular weight fusions (full length P28 and octamer) proved to be the most immunogenic. It may be that the immune response has been promoted by the carrier TetC providing additional T-cell helper epitopes [Francis *et al.* Nature 330: 168-170, 1987]. By week 4 all the mice immunized with cells carrying pTECH1-P28 responded to both TetC and also the full length P28 protein following i/v immunization. Mice immunized orally also responded to TetC and P28, although not all the mice responded to P28. It may well be that the response to P28 could be improved by boosting. Improved constructs consisting of codon optimised hinge regions, codon optimised P28, and

The E7 gene was obtained from plasmid pGEX16E7 (S.A. Comerford *et al.* J Virology, 65, 4681-90 1991). The gene in this plasmid is flanked by two restriction sites: a 3' BamHI site and a 5' EcoRI site. pGEX16E7 DNA was digested with EcoRI and blunt ended by a filling up reaction using Sequenase (DNA polymerase from USB). It was then digested with BamHI to release the 0.3 Kbp full length E7 gene.

5 The gel purified gene was ligated to BamHI-EcoRV double digested pTECH2 and this ligation mixture used to transform competent E. coli HB101 bacteria.

Recombinant colonies were selected by colony blotting using two monoclonal antibodies against HPV16 E7 protein as probes, namely 6D and 4F (R.W. Tindle, *et al* J Gen. Vir. 71,1347-54 1990). One of these colonies, named pTE79, was chosen for further analysis.

10 Protein extracts from pTE79 transformed E. coli grown in both aerobic and anaerobic conditions were prepared and analyzed by SDS-PAGE and Western blotting. Growth in anaerobic conditions resulted in expression of a recombinant molecule of about 60 KDa which reacted with monoclonal antibodies 6D and 4F and a rabbit polyclonal serum against Tetanus fragment C.

15 EXAMPLE 7

Construction of pTECH2-gD

An immunologically important antigen from herpes simplex virus type 1 [HSV1] is glycoprotein D, termed gD1 (R.J. Watson *et al* Science 218, 381-383 1982). A truncated gD1 gene cassette, lacking the transmembrane and cytoplasmic domains aa26-340, was synthesized by PCR. The PCR primers used are shown in Table 3. The forward primer was designed to encode the N-terminus of the mature protein and the reverse primer encoded the amino acids immediately 5' to the transmembrane domain. In addition the primers were tailored with BamHI and SpeI restriction sites respectively. The template for the PCR reaction was the plasmid pRWFG [a HSV1 gD BamHI-J clone from strain Patton in pBR322; a kind gift from Dr. T. Minson, Cambridge University]. The amplification product was digested with BamHI and SpeI and cloned into pTECH2 which had previously been digested with the respective enzymes.

Expression of the TetC-gD1 fusion protein was assessed by SDS-PAGE and Western blotting of bacterial strains harbouring the constructs. The Western blots were probed with either anti-TetC polyclonal sera or a monoclonal antibody directed against amino acids 11-19 of the mature gD [designated LP16, obtained from Dr. T. Minson, Cambridge].

10 The fusion protein is expressed as a 85kDa band visible on Western blots together with lower molecular weight bands down to 50kDa in size. The lower molecular weight bands could correspond to proteolytic cleavage products of gD or represent the products of premature translational termination within the coding region of gD due to ribosomal pausing. The fusion protein is expressed in the salmonella strains SL5338 and SL3261.

35 EXAMPLE 8

Construction of pTECH2-FMDV/SIV Reptitopes

Peptides from the foot and mouth disease virus (FMDV; serotype A12) viral protein 1 [VP1; aa136-159] and the V2 loop from simian immunodeficiency virus [SIV] env loop protein [gp120; aa171-190] were cloned into pTECH2 (M.P. Broekhuijsen *et al* J. Gen. Virol. 68, 3137-45 1987; K.A. Kent *et al.* AIDS Res. and Human Retro. 8:1147-1151 1992).

40 Complementary oligonucleotides encoding the peptides were designed with a codon selection for optimal expression in E. coli [H. Grosjean *et al* Gene, 18, 199-209, 1982]. The oligonucleotides are shown in Table 3. The oligonucleotides were tailored with BglII and SpeI cohesive ends which were generated upon annealing and cloned into pTECH2 which had previously been digested with BamHI and SpeI (Figure 3). Dimeric, tetrameric and octameric fusions of these peptides were constructed as described previously.

Expression of the TetC-fusions was assessed by SDS-PAGE and Western blotting with a polyclonal sera directed against TetC and monoclonal antibodies directed against either the FMDV or the SIV epitopes. The FMDV and SIV

position of a particular epitope in the TetC-Epitope A-Epitope B fusion on its expression level, stability, and immunogenicity, the converse combinations have also been constructed i.e. TetC-Epitope B-Epitope A, as is shown in Figure 11. "Heteromers" constructed in this way are TetC-P28 dimer-SIV dimer, TetC-SIV dimer-P28 dimer, TetC-P28 tetramer-SIV tetramer and TetC-SIV tetramer-P28 tetramer.

Expression of the tripartite fusions were evaluated by SDS-PAGE and Western blotting using the antibody reagents described above. These heteromer constructs are all expressed in the *Salmonella* strains SL5338 and SL3261, but intriguingly the expression level and stability is greater in one dimer-dimer and tetramer-tetramer combination (TetC-gp120-P28) than the converse.

EXAMPLE 10

MATERIALS AND METHODS

Plasmids, Oligonucleotides, and the Polymerase Chain Reaction

The plasmid pTETnir15 directs the expression of fragment C from tetanus toxin under the control of the *nirB* promoter [Chatfield *et al.* *idem* Oxer *et al.* *idem*]. The TetC-hinge fusion vector pTECH1 was constructed from pTETnir15 by the polymerase chain reaction (PCR) described by Mullis *et al.*, 1986. PCR was performed using the high-fidelity thermostable DNA polymerase from *Pyrococcus furiosus*, which possesses an associated 3'-5' exonuclease proofreading activity [K.S. Lundberg *et al.* *Gene* 108: 1-6, 1991]. The amplification reaction was performed according to the manufacturer's instructions (Stratagene).

Bacterial Strains

The bacterial strains used were *E. coli* TG2 (recA; [J. Sambrook *et al.* Molecular cloning: a laboratory manual. Cold Spring Harbor, New York, 1989]), *S. typhimurium* SL5338 (*galE* *r⁻m⁺* [A. Brown *J. Infect. Dis.* 155: 86-92, *et al.* *J. Infect. Dis.* 155: 86-92, 1987]) and SL3261 (*aroA*; [S.K. Hoiseth *et al.* *Nature* 291, 238-9, 1981]). Bacteria were cultured in either L or YT broth and on L-agar with ampicillin (50 µg/ml) if appropriate. Plasmid DNA prepared in *E. coli* was first modified by transformation into SL5338 to increase the efficiency of electroporation into the SL3261 *aroA* (*r⁻m*) vaccine. For electroporation, cells growing in mid-log phase were harvested and washed in half the initial culture volume of ice-cold water, 1/10 volume of ice-cold glycerol (10%), and finally the cells were resuspended to a concentration of 10¹⁰ cells/ml in ice-cold glycerol (10%). To a pre-chilled cuvette was added a mix of 60 µl cells and 100 ng of plasmid DNA. The cells were pulsed using the Porator from Invitrogen (settings: voltage=1750 µV, capacitance = 40 µF, resistance = 500). Prewarmed L-broth supplemented with 20 mM glucose was added immediately and the cells grown at 37°C with gentle shaking for 1-1.5 h. The cells were then plated on L-agar plates containing ampicillin and incubated at 37°C for 16 h.

SDS-PAGE and Western Blotting

Expression of the TetC fusions was tested by SDS-PAGE and Western blotting. Cells growing in mid-log phase with antibiotic selection were harvested by centrifugation and the proteins fractionated by 10% SDS-PAGE. The proteins were transferred to a nitrocellulose membrane by electroblotting and reacted with either a polyclonal rabbit antiserum directed against TetC or the full length P28 protein. The blots were then probed with goat anti-rabbit-Ig conjugated to horseradish peroxidase (Dako, UK) and developed with 4-chloro-1-naphthol.

Glutathione-Agarose Affinity Purification

Bacterial cells expressing the TetC full length P28 gene fusion were grown to log phase, chilled on ice, and harvested by centrifugation at 2500Xg for 15 min at 4°C. The cells were resuspended in 1/15th the original volume of ice-cold phosphate buffered saline (PBS) and lysed by sonication in a MSE Soniprep. The insoluble material was removed by centrifugation and to the supernatant was added 1/6 volume of a 50% slurry of pre-swollen glutathione agarose.

Animals

Female BALB/c mice were purchased from Harlan Olac UK Blackthorn, Bicester, UK, and used when at least 8 weeks of age.

Inoculations and viable counting of organ homogenates

Bacteria were grown in tryptic soy broth (Oxoid) supplemented with 100 µg/ml ampicillin as required. For intravenous inoculation, stationary cultures were diluted in PBS and animals were given approx. 10^6 cfu in a lateral tail vein in 0.2 ml. For oral inoculation, bacteria were grown in shaken overnight cultures, concentrated by centrifugation, and animals received approximately 5×10^9 cfu in 0.2 ml intragastrically via a gavage tube. The inoculum doses were checked by viable counts on tryptic soy agar. For viable counts on organ homogenates, groups of 3 mice were sacrificed at intervals, the livers and spleen and (for orally inoculated mice) a pool of mesenteric lymph nodes were homogenised separately in 10 ml distilled water in a Colworth stomacher [C.E. Hormaeche Immunology 37, 311-318, 1979] and viable counts performed on tryptic soy agar supplemented with 100 µg/ml ampicillin.

Measurement of antibody responses

Antibodies were measured by solid phase immunoassay. 96-well-flat bottomed plates were coated with either 0.1 µg of TetC (a kind gift from Dr N Fairweather, the Wellcome Foundation, Beckenham UK) or 1 µg of recombinant P28 (a kind gift from Dr R Pierce, Pasteur Institute, Lille, France) in 100 µl of 0.1 M carbonate buffer, pH 9.6. After overnight incubation at 4°C the plates were incubated for 1 h at 37°C. Blocking of non-specific binding sites was carried out by incubation with 200 µl of 2% casein (BDH, Poole, UK) in PBS pH 7.0 for 1 h at 37°C. Plates were washed three times with 0.05% Tween 20 (Sigma) in PBS with a semiautomatic ELISA washer (Titertek, Flow/ICN, Herts UK). 100 µl of sera from inoculated mice diluted 1:20 in 2% casein was added to each well and the plates were incubated for one hour at 37°C. The plates were washed as above and 100 µl of horse radish peroxidase conjugated goat antimouse immunoglobulins (Dako, Bucks UK), diluted according to the manufacturer's instructions in 2% casein in PBS, was added to each well and incubated for one hour at 37°C. The plates were washed as above and three more washes were given with PBS alone. The plates were developed using 3,3',3,3'-tetramethylbenzidine dihydrochloride (Sigma) according to the manufacturer's instructions using phosphate/citrate buffer, pH 5.0 and 0.02% hydrogen peroxide. The plates were incubated for 10-15 min at 37°C after which the reaction was stopped with 25 µl 3M H₂SO₄ (BDH). The plates were read in an ELISA reader at 450 nm.

Measurement of T-cell responses

Spleens from mice vaccinated 6 months in advance were removed aseptically and single cell suspensions were prepared by mashing the spleens through a stainless steel sieve with the help of a plastic plunger. Cells were washed once in RPMI1640 medium (Flow/ICN) at 300xg and incubated in Gey's solution to lyse the red cells. White cells were washed twice more as above and resuspended in complete medium, i.e. RPMI1640 supplemented with 100 U/ml penicillin G (Flow/ICN), 100 µg/ml streptomycin (Flow/ICN), 2×10^{-5} M B-mercapto-ethanol (Sigma), 1mM N-(2-hydroxyethyl)-piperazine-N'-(2-ethanesulphonic acid) (HEPES) (Flow/ICN) and 10% heat inactivated newborn bovine serum (Northumbria Biolabs, Northumberland, UK). For isolation of T-cells, spleen cells were treated as above and after lysis of red cells the white cells were resuspended in warm (37°C) RPMI1640 and passed through a Wigzell glass bead column [H. Wigzell, *et al* Scand. J. Immunol 1: 75-87, 1972].

Cells were plated at 2×10^6 /ml in a final volume of 200 µl of complete medium in 96-well plates in the presence of the relevant antigens. These were either an alkali-treated whole cell soluble extract of *S. typhimurium* C5 prepared as described in Villarreal *et al*. [Microbial Pathogenesis 13: 305-315, 1992] at 20 µg/ml final concentration; TetC at 10 µg/ml; recombinant *Schistosoma mansoni* P28 at 50 µg/ml; and *S. mansoni* whole adult worm extract (a kind gift from Dr D Dunne, Cambridge University) at 20 µg/ml. Cells were incubated in a 95% humidity, 5% CO₂, 37°C atmosphere.

cells/well CTLL-2(IL-2 dependent) in 50 µl of medium. CTLL-2 cells were obtained from Dr J Ellis, University College, London UK and maintained in RPMI1640 supplemented as above, substituting the newborn bovine serum for foetal bovine serum. After 20 h, 20 µl of MTT at a concentration of 5 mg/ml in PBS were added. MTT transformation was measured as indicated elsewhere [Tada *et al.* J. Immunol. Methods 93: 157-165, 1986]. results were expressed as the mean of the optical density of triplicates read at 570 nm using a reference filter of 630 nm. Significance was determined by Student's t-test.

BACTERIAL SAMPLE DEPOSITS

Salmonella typhimurium strains SL3261-pTECH1, SL3261-pTECH1-P28, SL3261-pTECH2, SL3261-pTECH2-P28 Octamer and PTE79 have been deposited at the National Collection of Type Cultures, 61 Colindale Avenue, London, NW9 5HT, UK, on 15th July 1993 under Deposit Numbers NCTC 12831, NCTC 12833, 12832, 12834 and 12837 respectively.

TABLE 1

DNA SEQUENCES OF OLIGONUCLEOTIDES UTILISED IN THE CONSTRUCTION OF THE TETC-HINGE VECTORS

A). Primer 1. Sense PCR (21mer). (SEQ ID NO: 4)

SacII

5'AAA GAC TCC GCG GGC GAA GTT -3'

TETANUS TOXIN C FRAGMENT SEQ.

B).Primer 2. Anti-Sense PCR Primer (64mer). (SEQ ID NO: 5)

BamHI

STOP

SpeI

XbaI

HINGE REGION

5'- CTAT GGA TCC TTA ACT AGT GAT TCT AGA GCG CCC CGG CCC

GTC GTT GGT CCA ACC TTC ATC GGT -3'

TETANUS TOXIN C FRAGMENT SEQ. 3'-END

C). The pTECH2 Linker (SEQ ID NO: 6)

XbaI BamHI EcoRV HindIII SpeI Stop XBamHI*

5'-CTAGA GGATCC GATATC AAGCTT ACTAGT TAA T-3'

3'-T CCTAGG CTATAG TTCGAA TGATCA ATT ACTAG-5'

*This BamHI recognition sequence is now destroyed.

TABLE 2

5 T-Cell responses (IL-2/IL-4 production) elicited by alkali treated salmonella whole cell extract (C5NaOH), TetC, *Schistosoma mansoni* whole adult worm antigen (SWA), and recombinant P28 in mice immunised with SL3261(pTETnir15) or SL3261(pTECH1.P28).

Immunising strain	Stimulating antigen				
	none	C5NaOH	TetC	P28	SWA
10 SL3261. (pTETnir15)	2±4	67±5	41±1	0	0
SL3261 (pTECH1-P28)	6±2.6	109±10	50±8	25±8 p<0.001	17±6 p<0.01
Results expressed as (A ₅₇₀ -A ₆₃₀) x 1000±S.D.					

TABLE 3Oligonucleotide Sequences for HSV, FMDV, and SIV.HSV1 gD Gene

PCR Primer 1: 5'-AATGGATCCAAATATGCCCTGGCGGATGC-3'
(SEQ ID NO: 7)

PCR Primer 2: 5'-TTAACTAGTGTGTTTCGGGGTGGCCGGGGGAT-3'
(SEQ ID NO: 8)

FMDV VP1 Epitope

Oligo 1:
5'-GATCTAAATACTCTGCTTCTGGTTCTGGTGTTCGTGGTGAC
TTCGGTTCTCTGGCTCCGCGTGTGCTCGTCAGCTGA-3'
(SEQ ID NO: 9)

Oligo 2:
5'-TAGTCAGCTGACGAGCAACACGCGGAGCCAGAGAACCGAA
GTCACCACGAACACCAGAACCAGAAGCAGAGTATTTA-3'
(SEQ ID NO: 10)

SIV gp120 Epitope

Oligo 1:
5'-GATCTAACATGACCGGTCTGAAACGTGATAAAACCAAGAA
TACAACGAAACCTGGTACTCTACCA-3'
(SEQ ID NO: 11)

Oligo 2:
5'-CTAGTGGTAGAGTACCAGGTTTCGTTGTATTCTTTGGTTTT
ATCACGTTTCAGACCGGTCATGTTA-3'
(SEQ ID NO: 12)

Sm P28 Gene

PCR Primer 1: 5'-TAGTCTAGAATGGCTGGCGAGCATATCAAG-3'
(SEQ ID NO: 13)

PCR Primer 2: 5'-TTAGGATCCTTAGAAGGGAGTTGCAGGCCT-3'
(SEQ ID NO: 14)

Sm P28 Epitope

Oligo 1:
5'-GATCTAAACCGCAGGAAGAAAAAGAAAAATCACCAAGAAA
TCCTGAACGGCAAAA-3'
(SEQ ID NO: 15)

Oligo 2:
5'-CTAGTTTTGCCGTTTCAGGATTTCTTTGGTGATTTTTCTTTTCT
TCCTGCGGTTTA-3'
(SEQ ID NO: 16)

SEQUENCE LISTING

5 (1) GENERAL INFORMATION:

(i) APPLICANT:

(A) NAME: MEDEVA HOLDINGS BV
(B) STREET: CHURCHILL-LAAN 223
10 (C) CITY: AMSTERDAM
(E) COUNTRY: THE NETHERLANDS
(F) POSTAL CODE (ZIP): 1078 ED

(ii) TITLE OF INVENTION: VACCINES

15 (iii) NUMBER OF SEQUENCES: 20

(iv) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
20 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

(v) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: GB 9216317.9
(B) FILING DATE: 31-JUL-1992

25

(vi) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: GB 9306398.0
(B) FILING DATE: 26-MAR-1993

30

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 68 base pairs
(B) TYPE: nucleic acid
35 (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

40

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Escherichia coli

45

(ix) FEATURE:

(A) NAME/KEY: promoter
(B) LOCATION: 1..61

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

AATTCAGGTA AATTGATGT ACATCAAATG GTACCCCTTG CTGAATCCTT AAGGTAGGCG

60

55

GTAGGGCC

68

(2) INFORMATION FOR SEQ ID NO: 2:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 68 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

AATTCAGGTA AATTTGATGT ACATCAAATG GTACCCCTTG CTGAATCGTT AAGGTAGGCG

60

GTAGGGCC

68

(2) INFORMATION FOR SEQ ID NO: 3:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 60 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

CTACCGCCTA CCTTAACGAT TCAGCAAGGG GTACCATTTG ATGTACATCA AATTACCTG

60

(2) INFORMATION FOR SEQ ID NO: 4:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

AAAGACTCCG CGGGCGAAGT T

21

10

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 64 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

15

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

20

(iii) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

25

CTATGGATCC TTAAGTAGTG ATTCTAGAGG GCGGCGGCCC GTCGTTGGTC CAACCTTCAT

60

CGGT

64

30

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

35

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

40

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

45

CTAGAGGATC CGATATCAAG CTTACTAGTT AAT

33

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

50

55

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

AATGGATCCA AATATGCCCT GGCGGATGC

29

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

TAACTAGTGT TGTTCTGGGGT GGCCGGGGGA T

31

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 78 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

GATCTAAATA CTCTGCTTCT GGTCTGGTG TTCGTGGTGA CTCGGTTCT CTGGCTCCGC

60

GTGTTGCTCG TCAGCTGA

78

(2) INFORMATION FOR SEQ ID NO: 10:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 78 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

CTAGTCAGCT GACGAGCAAC ACGCGGAGCC AGAGAACCGA AGTCACCACG AACACCAGAA 60
CCAGAAGCAG AGTATTTA 78

(2) INFORMATION FOR SEQ ID NO: 11:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 66 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

GATCTAACAT GACCGGTCTG AAACGTGATA AAACCAAAGA ATACAACGAA ACCTGGTACT 60
CTACCA 66

(2) INFORMATION FOR SEQ ID NO: 12:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 66 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

CTAGTGGTAG AGTACCAGGT TTCGTTGTAT TCTTTGGTTT TATCACGTTT CAGACCGGTC 60

10

ATGTTA 66

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 30 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

20

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

TAGTCTAGAA TGGCTGGCGA GCATATCAAG 30

30

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

35

(A) LENGTH: 30 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

40

(iii) ANTI-SENSE: NO

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

TTAGGATCCT TAGAAGGGAG TTGCAGGCCT 30

(2) INFORMATION FOR SEQ ID NO: 15:

50

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 57 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

55

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

GATCTAAACC GCAGGAAGAA AAAGAAAAAA TCACCAAAGA AATCCTGAAC GGCAAAA

57

(2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 57 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

CTAGTTTTCG CGTTCAGGAT TTCTTTGGTG ATTTTTCCTT TTTCTTCCTG CGGTTTA

57

(2) INFORMATION FOR SEQ ID NO: 17:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3754 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

TTCAGGTAAA TTGATGTAC ATCAAATGGT ACCCCTTGCT GAATCGTTAA GGTAGGCGGT

60

AGGGCCCCAGA TCTTAATCAT CCACAGGAGA CTTTCTGATG AAAACCTTG ATTGTTGGGT

120

	CGACAACGAA GAAGACATCG ATGTTATCCT GAAAAAGTCT ACCATTCTGA ACTTGGACAT	180
	CAACAACGAT ATTATCTCCG ACATCTCTGG TTTCAACTCC TCTGTTATCA CATATCCAGA	240
5	TGCTCAATTG GTGCCGGGCA TCAACGGCAA AGCTATCCAC CTGGTTAACA ACGAATCTTC	300
	TGAAGTTATC GTGCACAAGG CCATGGACAT CGAATACAAC GACATGTTCA ACAACTTCAC	360
10	CGTTAGCTTC TGGCTGCGCG TTCCGAAAGT TTCTGCTTCC CACCTGGAAC AGTACGGCAC	420
	TAACGAGTAC TCCATCATCA GCTCTATGAA GAAACACTCC CTGTCCATCG GCTCTGGTTG	480
	GTCTGTTTCC CTGAAGGGTA ACAACCTGAT CTGGACTCTG AAAGACTCCG CGGGCGAAGT	540
15	TCGTCAAGTC ACTTTCCGCG ACCTGCCGGA CAAGTTCAAC GCGTACCTGG CTAACAAATG	600
	GGTTTTTCATC ACTATCACTA ACGATCGTCT GTCTTCTGCT AACCTGTACA TCAACGGCGT	660
	TCTGATGGGC TCCGCTGAAA TCACTGGTCT GGGCGCTATC CGTGAGGACA ACAACATCAC	720
20	TCTTAAGCTG GACCGTTGCA ACAACAACAA CCAGTACGTA TCCATCGACA AGTTCCGTAT	780
	CTTCTGCAAA GCACTGAACC CGAAAGAGAT CGAAAACTG TATACCAGCT ACCTGTCTAT	840
	CACCTTCCTG CGTGACTTCT GGGGTAACCC GCTGCGTTAC GACACCGAAT ATTACCTGAT	900
25	CCCGGTAGCT TCTAGCTCTA AAGACGTTCA GCTGAAAAAC ATCACTGACT ACATGTACCT	960
	GACCAACGCG CCGTCTTACA CTAACGGTAA ACTGAACATC TACTACCGAC GTCTGTACAA	1020
30	CGGCCTGAAA TTCATCATCA AACGCTACAC TCCGAACAAC GAAATCGATT CTTTCGTAA	1080
	ATCTGGTGAC TTCATCAAAC TGTACGTTTC TTACAACAAC AACGAACACA TCGTTGGTTA	1140
	CCCGAAAGAC GGTAACGCTT TCAACAACCT GGACAGAATT CTGCGTGTG GTTACAACGC	1200
35	TCCGGGTATC CCGCTGTACA AAAAAATGGA AGCTGTAAA CTGCGTGACC TGAAAACCTA	1260
	CTCTGTTTCA CTGAAACTGT ACGACGACAA AAACGCTTCT CTGGGTCTGG TTGGTACCCA	1320
	CAACCGTCAG ATCGGTAACG ACCCGAACCG TGACATCCTG ATCGCTTCTA ACTGGTACTT	1380
40	CAACCACCTG AAAGACAAAA TCCTGGGTTG CGACTGGTAC TTCGTTCCGA CCGATGAAGG	1440
	TTGGACCAAC GACGGGCCGG GGCCCTCTAG AATCACTAGT TAAGGATCCG CTAGCCCGCC	1500
	TAATGAGCGG GCTTTTTTTT CTCGGGCAGC GTTGGGTCTT GGCCACGGGT GCGCATGATC	1560
45	GTGCTCCTGT CGTTGAGGAC CCGGCTAGGC TGGCGGGGTT GCCTTACTGG TTAGCAGAAT	1620
	GAATCACC GA TACGCGAGCG AACGTGAAGC GACTGCTGCT GCAAAACGTC TGCGACCTGA	1680
50	GCAACAACAT GAATGGTCTT CGGTTTCCGT GTTTCGTAAA GTCTGGAAAC GCGGAAGTCA	1740
	GCGCTCTTCC GCTTCCTCGC TCACTGACTC GCTGCGCTCG GTCGTTCCGG TCGGGCGAGC	1800

55

	GGTATCAGCT CACTCAAAGG CGGTAATACG GTTATCCACA GAATCAGGGG ATAACGCAGG	1860
5	AAAGAACATG TGAGCAAAAG GCCAGCAAAA GCCCAGGAAC CGTAAAAGG CCGCGTTGCT	1920
	GGCGTTTTTC CATAGGCTCC GCCCCCTGA CGAGCATCAC AAAAATCGAC GCTCAAGTCA	1980
	GAGGTGGCGA AACCCGACAG GACTATAAAG ATACCAGGCG TTTCCCCCTG GAAGCTCCCT	2040
10	CGTGCGCTCT CCTGTTCCGA CCCTGCCGCT TACCGGATAC CTGTCCGCCT TTCTCCCTTC	2100
	GGGAAGCGTG GCGCTTTCTC AATGCTCAGC CTGTAGGTAT CTCAGTTCGG TGTAGGTCGT	2160
	TCGCTCCAAG CTGGGCTGTG TGCACGAACC CCCCCTCAG CCCGACCGCT GCGCCTTATC	2220
15	CGGTA ACTAT CGTCTTGAGT CCAACCCGGT AAGACACGAC TTATCGCCAC TGGCAGCAGC	2280
	CACTGGTAAC AGGATTAGCA GAGCGAGGTA TGTAGGCGGT GCTACAGAGT TCTTGAAGTG	2340
	GTGGCCTAAC TACGGCTACA CTAGAAGGAC AGTATTGGT ATCTGCGCTC TGCTGAAGCC	2400
20	AGTTACCTTC GGAAAAAGAG TTGGTAGCTC TTGATCCGGC AAACAAACCA CCGCTGGTAG	2460
	CGGTGGTTTT TTTGTTTGCA AGCAGCAGAT TACGCCGAGA AAAAAGGAT CTCAAGAAGA	2520
25	TCCTTTGATC TTTTCTACGG GGTCTGACGC TCAGTGGAAAC GAAAACTCAC GTTAAGGGAT	2580
	TTTGGTCATG AGATTATCAA AAAGGATCTT CACCTAGATC CTTTAAATT AAAAATGAAG	2640
	TTTTAAATCA ATCTAAAGTA TATATGAGTA AACTTGGTCT GACAGTTACC AATGCTTAAT	2700
30	CAGTGAGGCA CCTATCTCAG CGATCTGTCT ATTTCTGTTCA TCCATAGTTG CCTGACTCCC	2760
	CGTCGTGTAG ATA ACTACGA TACGGGAGGG CTTACCATCT GGCCCCAGTG CTGCAATGAT	2820
	ACCGCGAGAC CCACGCTCAC CGGCTCCAGA TTTATCAGCA ATAAACCAGC CAGCCGGAAG	2880
35	GGCCGAGCCG AGAAGTGGTC CTGCAACTTT ATCCGCCTCC ATCCAGTCTA TTAATTGTTG	2940
	CCGGGAAGCT AGAGTAAGTA GTTCGCCAGT TAATAGTTTG CGCAACGTTG TTGCCATTGC	3000
	TGCAGGCATC GTGGTGTAC GTCGTCGTT TGGTATGGCT TCATTAGCT CCGGTTCCCA	3060
40	ACGATCAAGG CGAGTTACAT GATCCCCCAT GTTGTGCAAA AAAGCGGTGA GCTCCTTCGG	3120
	TCCTCCGATC GTTGTGAGAA GTAAGTTGGC CGCAGTGTTA TCACTCATGG TTATGGCAGC	3180
45	ACTGCATAAT TCTCTTACTG TCATGCCATC CGTAAGATGC TTTTCTGTGA CTGGTGAGTA	3240
	CTCAACCAAG TCATTCTGAG AATAGTGTAT GCGGCGACCG AGTTGCTCTT GCCCGGCGTC	3300
	AACACGGGAT AATACCGCGC CACATAGCAG AACTTTAAAA GTGCTCATCA TTGAAAAACG	3360
50	TTCTTCGGGG CGAAAACTCT CAAGGATCTT ACCGCTGTTG AGATCCAGTT CGATGTAACC	3420
	CACTCGTGCA CCCAACTGAT CTTACGCATC TTTTACTTTC ACCAGCGTTT CTGGGTGAGC	3480

AAAACAGGA AGGCAAAATG CCGCAAAAAA GGAATAAGG GCGACACGGA AATGTTGAAT 3540
 ACTCATACTC TTCCTTTTTT AATATTATTG AAGCATTAT CAGGGTTATT GTCTCATGAG 3600
 5 CCGATACATA TTTGAATGTA TTTAGAAAAA TAAACAAATA GGGGTTCGCG GCACATTTCC 3660
 CCGAAAAGTG CCACCTGACG TCTAAGAAAC CATTATTATC ATGACATTAA CCTATAAAAA 3720
 10 TAGGCGTATC ACGAGGCCCT TTCGTCTTCA AGAA 3754

(2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3769 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

TTCAGGTAAA TTTGATGTAC ATCAAATGGT ACCCCTTGCT GAATCGTTAA GGTAGGCGGT 60
 AGGGCCCAGA TCTTAATCAT CCACAGGAGA CTTTCTGATG AAAACCTTG ATTGTTGGGT 120
 30 CGACAACGAA GAAGACATCG ATGTTATCCT GAAAAAGTCT ACCATTCTGA ACTTGGACAT 180
 CAACAACGAT ATTATCTCCG ACATCTCTGG TTTCAACTCC TCTGTTATCA CATATCCAGA 240
 35 TGCTCAATTG GTGCCGGGCA TCAACGGCAA AGCTATCCAC CTGGTTAACA ACGAATCTTC 300
 TGAAGTTATC GTGCACAAGG CCATGGACAT CGAATACAAC GACATGTTCA ACAACTTCAC 360
 CGTTAGCTTC TGGCTGCGCG TTCCGAAAGT TTCTGCTTCC CACCTGGAAC AGTACGGCAC 420
 40 TAACGAGTAC TCCATCATCA GCTCTATGAA GAAACACTCC CTGTCCATCG GCTCTGGTTG 480
 GTCTGTTTCC CTGAAGGGTA ACAACCTGAT CTGGACTCTG AAAGACTCCG CGGGCGAAGT 540
 TCGTCAGATC ACTTTCCGCG ACCTGCCGGA CAAGTTCAAC GCGTACCTGG CTAACAAATG 600
 45 GGTITTCATC ACTATCACTA ACGATCGTCT GTCTTCTGCT AACCTGTACA TCAACGGCGT 660
 TCTGATGGGC TCCGCTGAAA TCACTGGTCT GGGCGCTATC CGTGAGGACA ACAACATCAC 720
 50 TCTTAAGCTG GACCGTTGCA ACAACAACAA CCAGTACGTA TCCATCGACA AGTTCGGTAT 780

	CACCTTCCTG CGTGACTTCT GGGGTAACCC GCTGCGTTAC GACACCGAAT ATTACCTGAT	900
5	CCCCGTAGCT TCTAGCTCTA AAGACGTTCA GCTGAAAAAC ATCACTGACT ACATGTACCT	960
	GACCAACGCG CCGTCCTACA CTAACGGTAA ACTGAACATC TACTACCGAC GTCTGTACAA	1020
	CGGCCTGAAA TTCATCATCA AACGCTACAC TCCGAACAAC GAAATCGATT CTTTCGTTAA	1080
10	ATCTGGTGAC TTCATCAAAC TGTACGTTTC TTACAACAAC AACGAACACA TCGTTGGTTA	1140
	CCCCAAAGAC GGTAAACGCTT TCAACAACCT GGACAGAATT CTGCGTGTTG GTTACAACGC	1200
	TCCGGGTATC CCGCTGTACA AAAAAATGGA AGCTGTTAAA CTGCGTGACC TGAAAACCTA	1260
15	CTCTGTTTAC CTGAAACTGT ACGACGACAA AAACGCTTCT CTGGGTCTGG TTGGTACCCA	1320
	CAACGGTCAG ATCGGTAACG ACCCGAACCG TGACATCCTG ATCGCTTCTA ACTGGTACTT	1380
	CAACCACCTG AAAGACAAAA TCCTGGGTTG CGACTGGTAC TTCGTCCGA CCGATGAAGG	1440
20	TTGGACCAAC GACGGGCCGG GCCCTCTAG AGGATCCGAT ATCAAGCTTA CTAGTTAATG	1500
	ATCCGCTAGC CCGCCTAATG AGCGGGCTTT TTTTCTCGG GCAGCGTTGG GTCCTGGCCA	1560
25	CGGGTCGCCA TGATCGTGCT CCTGTCTTG AGGACCCGGC TAGGCTGGCG GGGTTGCCTT	1620
	ACTGGTTAGC AGAATGAATC ACCGATACGC GAGCGAACGT GAAGCGACTG CTGCTGCAAA	1680
	ACGTCTGCCA CCTGAGCAAC AACATGAATG GTCTTCGGTT TCCGTGTTTC GTAAAGTCTG	1740
30	GAAACGCGGA AGTCAGCGCT CTTCCGCTTC CTCGCTCACT GACTCGCTGC GCTCGGTCTG	1800
	TCCGCTGCCG CGAGCGGTAT CAGCTCACTC AAAGGCGGTA ATACGGTTAT CCACAGAATC	1860
	AGGGGATAAC GCAGGAAAGA ACATGTGAGC AAAAGGCCAG CAAAAGGCCA GGAACCGTAA	1920
35	AAAGGCCGCG TTGCTGGCGT TTTTCCATAG GCTCCGCCCC CCTGACGAGC ATCACAAAAA	1980
	TCGACGCTCA AGTCAGAGGT GGCAGAACCC GACAGGACTA TAAACATACC AGGCGTTTCC	2040
40	CCCTGGAAGC TCCCTCGTGC GCTCTCCTGT TCCGACCCTG CCGCTTACCG GATACCTGTC	2100
	CGCCTTTCTC CCTTCGGGAA GCGTGGCGCT TTCTCAATGC TCACGCTGTA GGTATCTCAG	2160
	TTCCGTGTAG GTCGTTGCT CCAAGCTGGG CTGTGTGCAC GAACCCCCCG TTCAGCCCGA	2220
45	CCGCTGCGCC TTATCCGGTA ACTATCGTCT TGAGTCCAAC CCGTAAGAC ACGACTTATC	2280
	GCCACTGGCA GCAGCCACTG GTAACAGGAT TAGCAGAGCG AGGTATGTAG GCGGTGCTAC	2340
	AGAGTTCTTG AAGTGGTGGC CTAACACGG CTACACTAGA AGGACAGTAT TTGGTATCTG	2400
50	CGCTCTGCTG AAGCCAGTTA CCTTCGGAAA AAGAGTTGGT AGCTCTTGAT CCGGCAAACA	2460
	AACCACCCT GGTAGCGGTG GTTTTTTGT TTGCAAGCAG CAGATTACGC GCAGAAAAAA	2520

55

AGGATCTCAA GAAGATCCTT TGATCTTTTC TACGGGGTCT GACGCTCAGT GGAACGAAAA 2580
 CTCACGTTAA GGGATTTTGG TCATGAGATT ATCAAAAAGG ATCTTCACCT AGATCCTTTT 2640
 5 AAATTAAAAA TGAAGTTTAA AATCAATCTA AAGTATATAT GAGTAAACTT GGTCTGACAG 2700
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 15 GTCTATTAAT TGTGCCCCG AAGCTAGAGT AAGTAGTTCG CCAGTTAATA GTTTGCGCAA 3000
 CGTTGTTGCC ATTGCTGCAG GCATCGTGGT GTCACGCTCG TCGTTTGGTA TGGCTTCATT 3060
 CAGCTCCGGT TCCCAACGAT CAAGGCGAGT TACATGATCC CCCATGTTGT GCAAAAAAGC 3120
 20 GGTAGCTCC TTCGGTCCTC CGATCGTTGT CAGAAGTAAG TTGGCCGCGAG TGTTATCACT 3180
 CATGGTTATG GCAGCACTGC ATAATTCTCT TACTGTCATG CCATCCGTAA GATGCTTTTC 3240
 TGTGACTGGT GAGTACTCAA CCAAGTCATT CTGAGAATAG TGTATGCGGC GACCGAGTTG 3300
 25 CTCTTGCCCC GCGTCAACAC GGGATAATAC CGCGCCACAT AGCAGAACTT TAAAAGTGCT 3360
 CATCATTGGA AAACGTTCTT CGGGGCGAAA ACTCTCAAGG ATCTTACCGC TGTTGAGATC 3420
 CAGTTCGATG TAACCCACTC GTGCCCCAA CTGATCTTCA GCATCTTTTA CTTTCACCAG 3480
 30 CGTTTCTGGG TGAGCAAAAA CAGGAAGGCA AAATGCCGCA AAAAAGGGAA TAAGGGCGAC 3540
 ACGGAAATGT TGAATACTCA TACTCTTCCT TTTTCAATAT TATTGAAGCA TTTATCAGGG 3600
 35 TTATTGCTC ATGAGCGGAT ACATATTTGA ATGTATTTAG AAAAATAAAC AAATAGGGGT 3660
 TCCGCGCACA TTTCCCGGAA AAGTGCCACC TGACGTCTAA GAAACCATTA TTATCATGAC 3720
 ATTAACCTAT AAAAATAGGC GTATCAGCAG GCCCTTTCGT CTTCAAGAA 3769

(2) INFORMATION FOR SEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 38 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

TCTAGAGGAT CCGATATCAA GCTTACTAGT TAATGATC

38

(2) INFORMATION FOR SEQ ID NO: 20:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

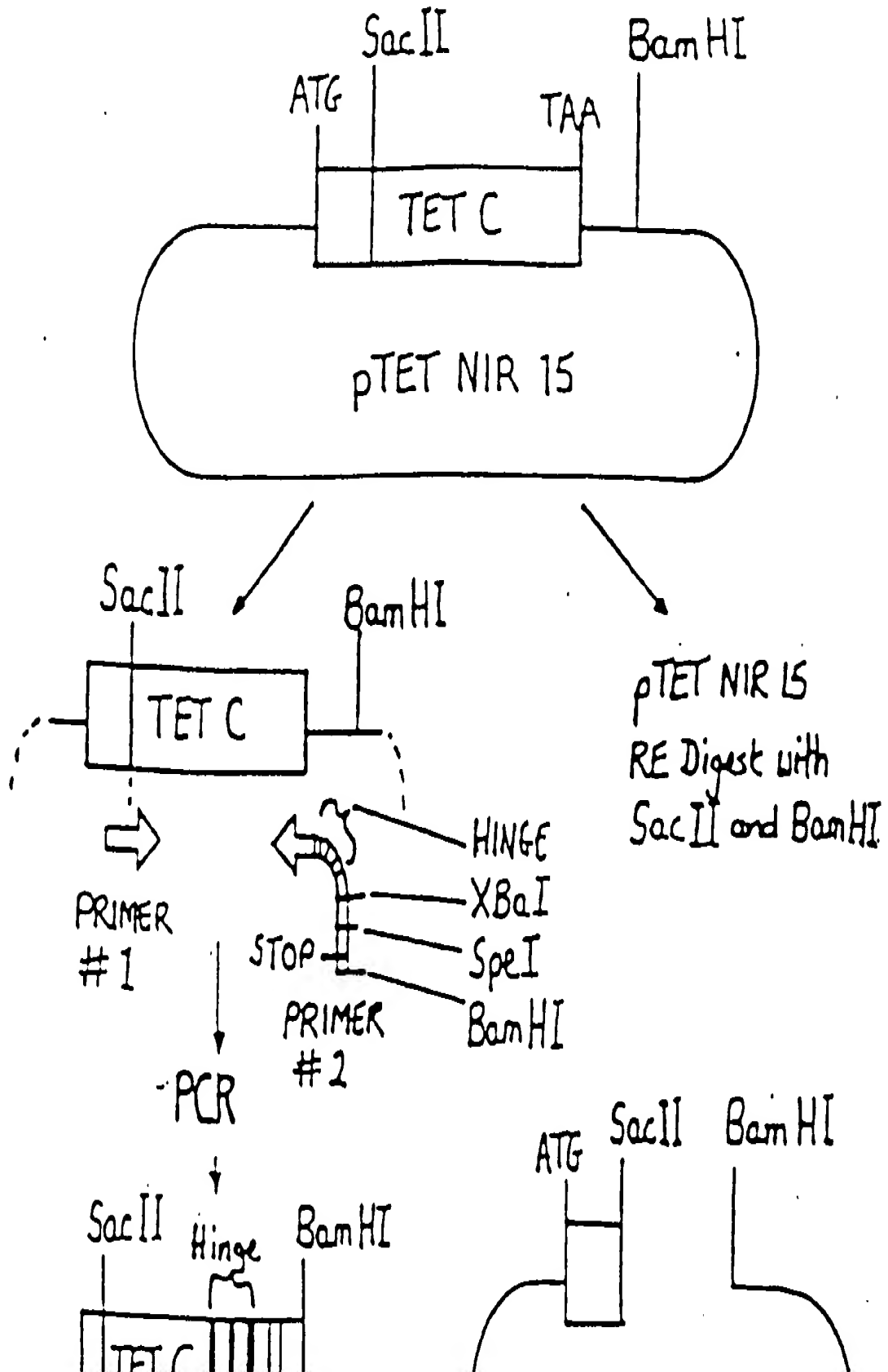
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

Gly Pro Gly Pro Ser Arg Gly Ser Asp Ile Lys Leu Thr Ser
1 5 10

Claims

1. A fusion protein, preferably in substantially pure form, the fusion protein comprising tetanus toxin fragment C linked at its C-terminal to a heterologous second protein.
2. A fusion protein according to claim 1 wherein the tetanus toxin C-fragment and the second protein are linked by a hinge region.
3. A fusion protein according to claim 1 or claim 2 wherein the second protein is an immunogen.
4. A fusion protein according to claim 3 wherein the second protein is an antigenic sequence derived from a virus, bacterium, fungus, yeast or parasite.
5. A fusion protein according to claim 4 wherein the second protein is an antigenic determinant of a pathogenic organism.
6. A fusion protein according to claim 5 wherein the second protein is an antigenic sequence derived from a type of human immuno-deficiency virus (HIV) such as HIV-1 or HIV-2, the CD4 receptor binding site from HIV, for example from HIV-1 or -2, hepatitis A or B virus, human rhinovirus such as type 2 or type 14, Herpes simplex virus, poliovirus type 2 or 3, foot-and-mouth disease virus (FMDV), rabies virus, rotavirus, influenza virus, coxsackie virus, human papilloma virus (HPV), for example the type 16 papilloma virus, the E7 protein thereof, and fragments containing the E7 protein or its epitopes; and simian immunodeficiency virus (SIV); Bordetella pertussis (e.g. P69 protein and filamentous haemagglutinin (FHA) antigens), Vibrio cholerae, Bacillus anthracis, and E.coli antigens such as E.coli heat labile toxin B subunit (LT-B), E.coli K88 antigens, and enterotoxigenic E.coli antigens; the cell surface antigen CD4, Schistosoma mansoni P28 glutathione S-transferase antigens (P28 antigens) and antigens of flukes, mycoplasma, roundworms, tapeworms, Chlamydia trachomatis, and malaria parasites, eg. parasites of the genus Plasmodium or babesia, for example Plasmodium falciparum, and peptides encoding immunogenic epitopes thereof.

7. A fusion protein according to claim 6 wherein the second protein is an antigen selected from the full length Schistosoma mansoni P28, oligomers (e.g. 2, 4 and 8-mers) of the immunogenic P28 aa 115-131 peptide (which contains both a B and T cell epitope), and human papilloma virus E7 protein, Herpes simplex antigens, foot and mouth disease virus antigens and simian immunodeficiency virus antigens.
8. A fusion protein according to any one of the preceding claims wherein the hinge region comprises a high proportion of proline and/or glycine amino acids.
9. A fusion protein according to claim 8 wherein the hinge region is composed entirely of proline and/or glycine amino acids.
10. A fusion protein according to claim 8 wherein the hinge region comprises one or more glycine-proline dipeptide units.
11. A fusion protein according to any one of the preceding claims wherein the hinge region contains up to about fifteen amino acids.
12. A fusion protein according to claim 11 wherein the hinge region contains at least 4 and preferably 6-14 amino acids.
13. A fusion protein according to claim 12 wherein the hinge region is a chain of four or more amino acids defining the sequence
-[X]_p-Pro-[Y]_q-Pro-[Z]_r-
wherein Pro is proline, X and Y are each glycine, or an amino acid having a non-bulky side chain; Z is any amino acid; p is a positive integer; q is a positive integer of from one to ten; and r is zero or a positive integer greater than zero.
14. A fusion protein according to any one of the preceding claims wherein the hinge region is defined by a carboxy-end protein of the tetanus toxin C-fragment or an amino-end portion of the second protein.
15. A vaccine composition comprising a fusion protein as defined in any one of the preceding claims and a pharmaceutically acceptable carrier.



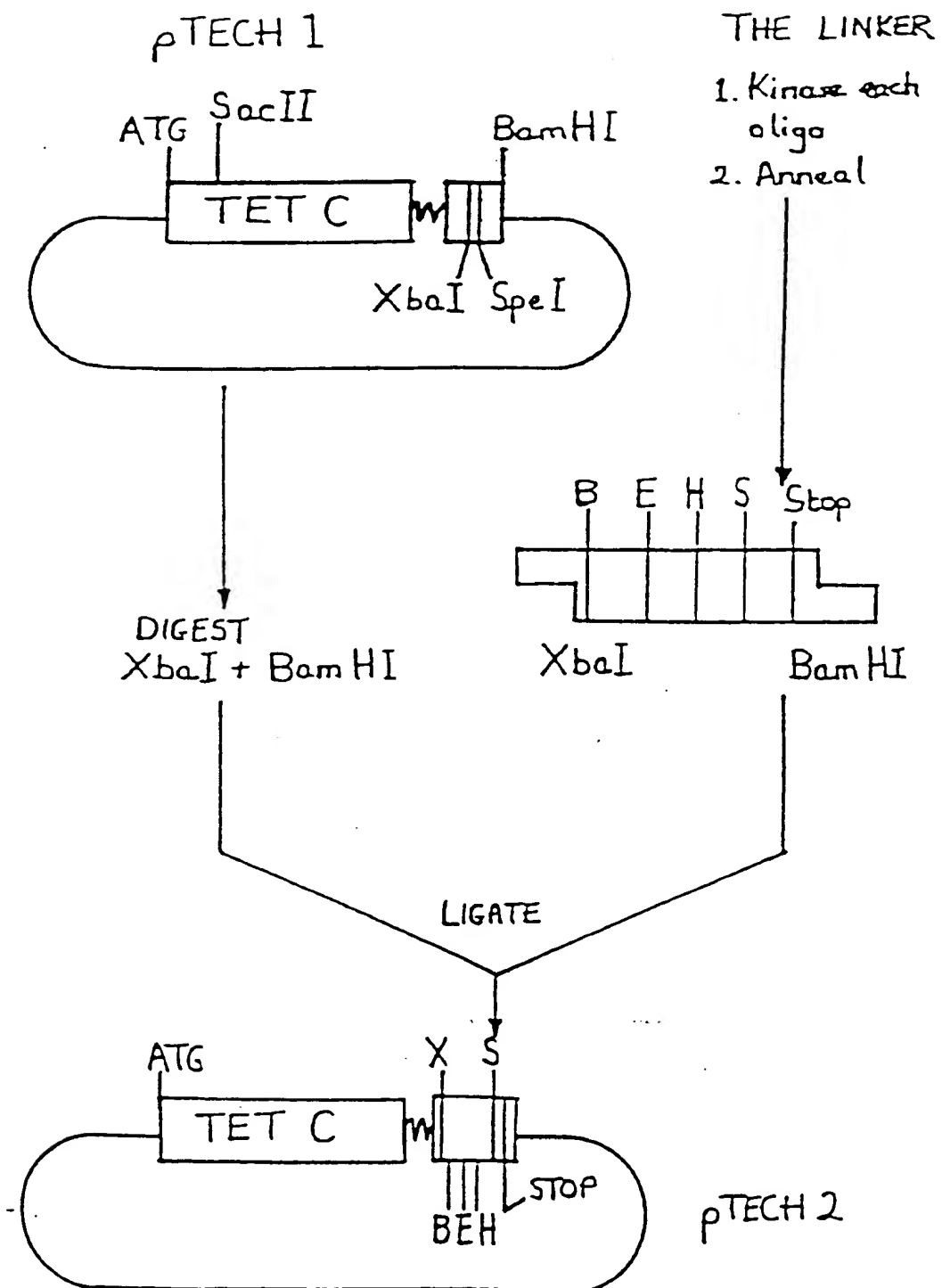


FIGURE 2

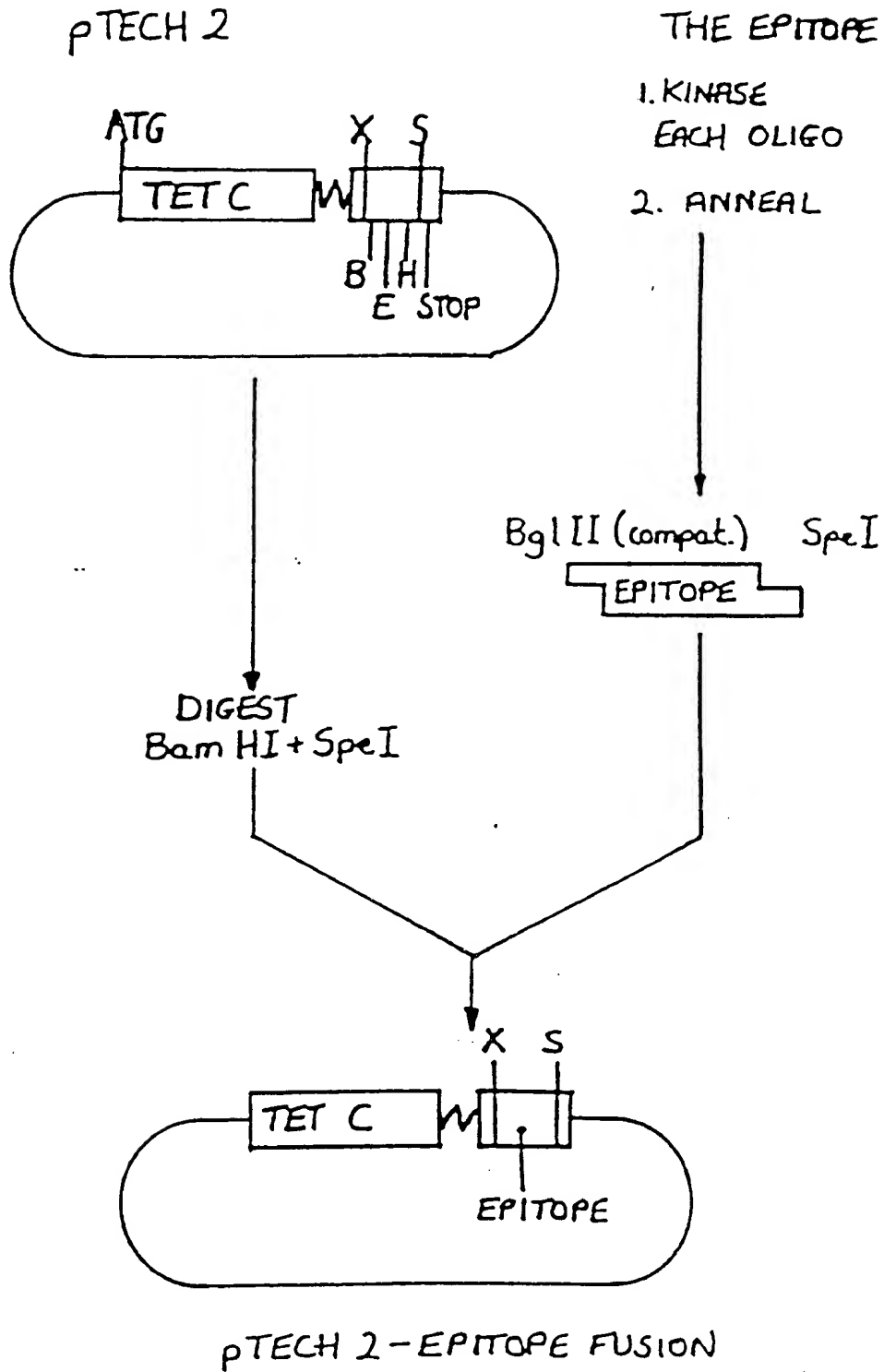
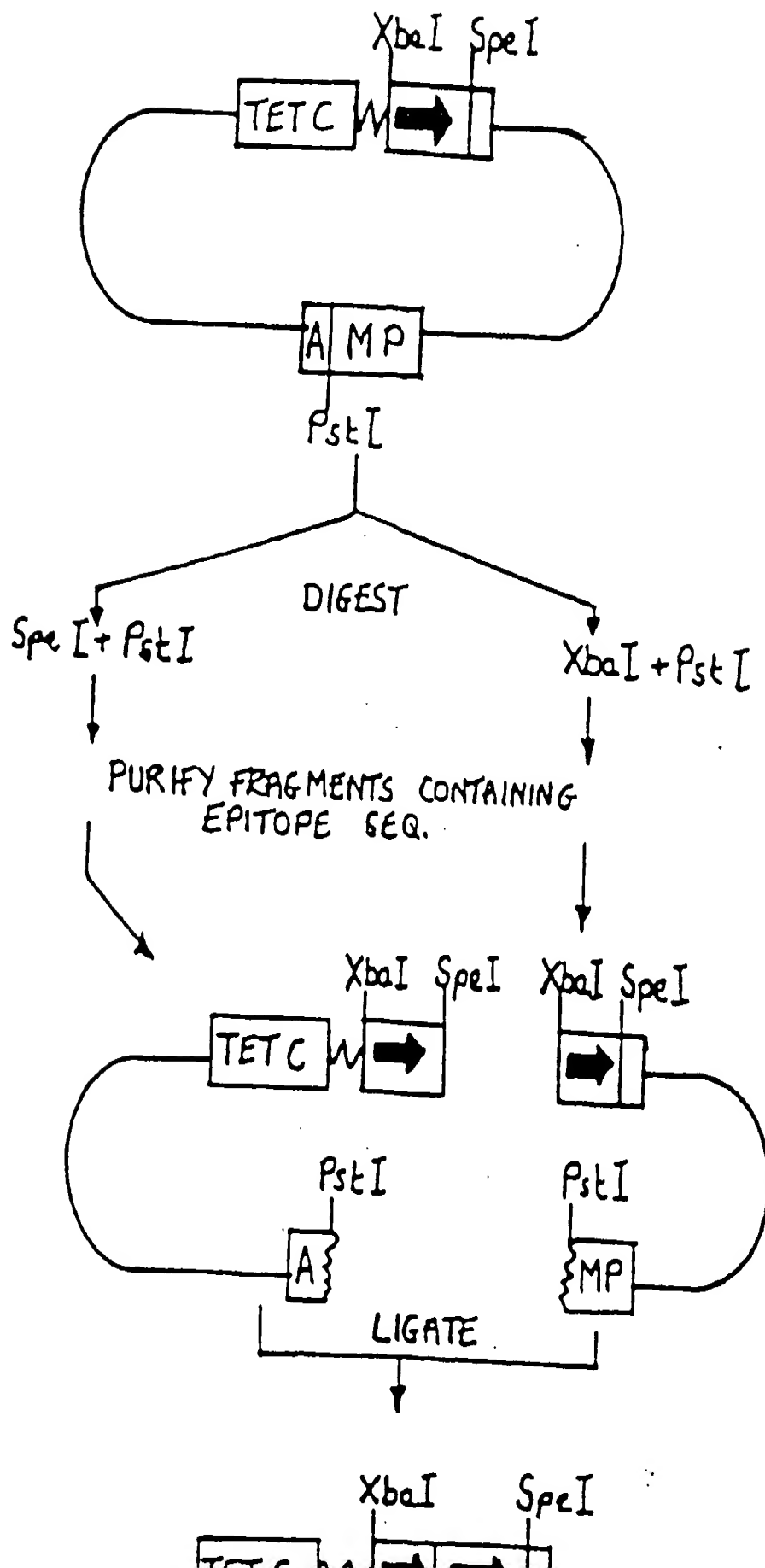


FIGURE 3



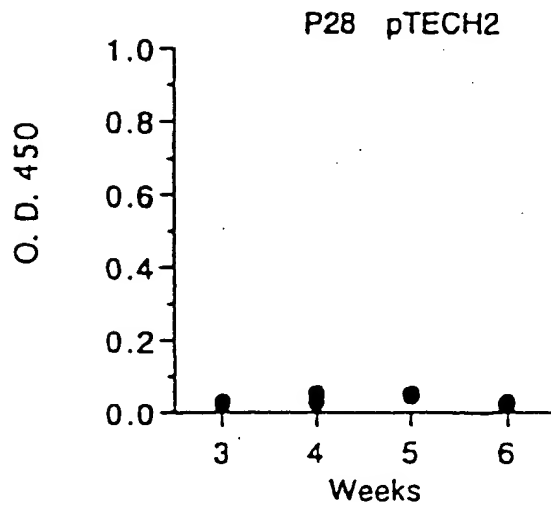
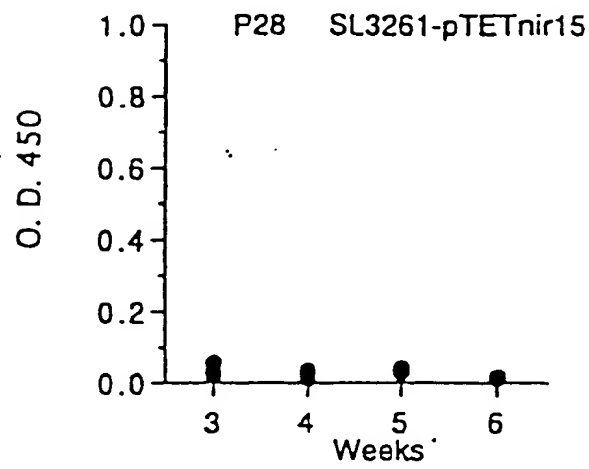
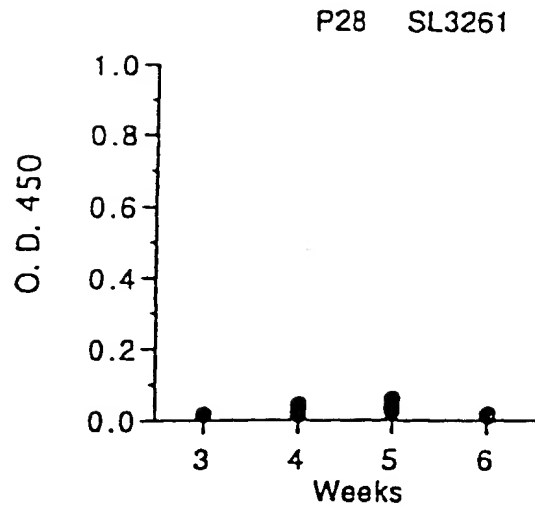


Figure 5

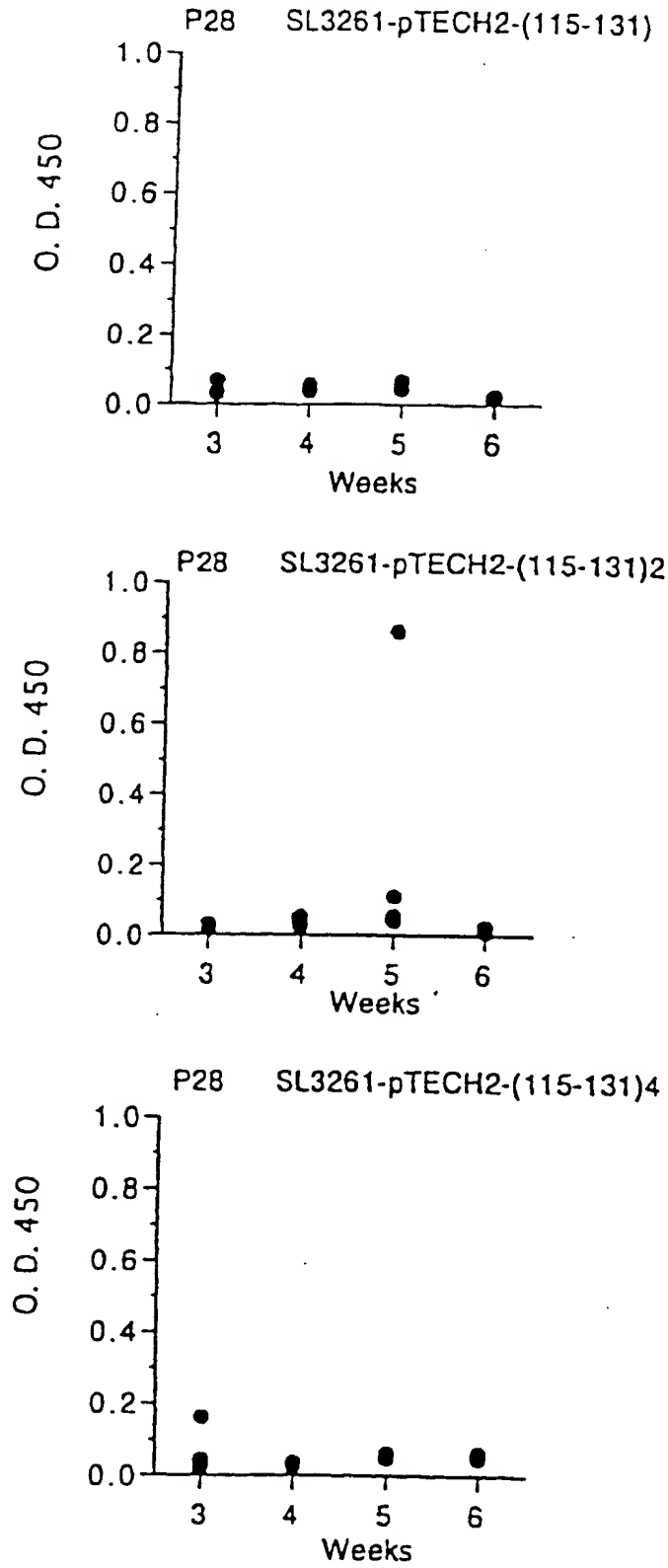


Figure 5 continued

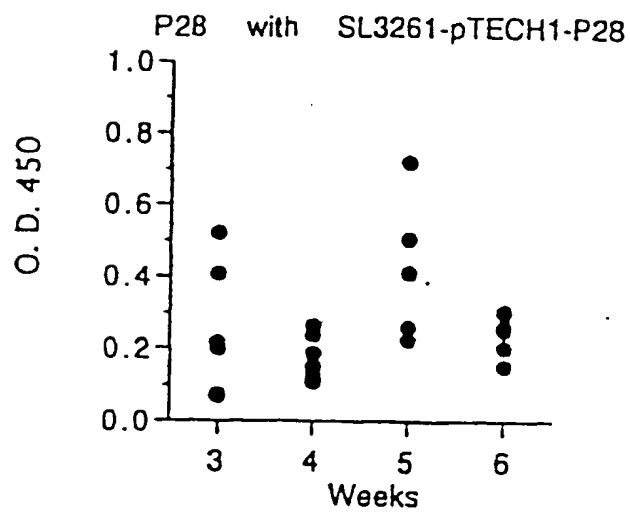
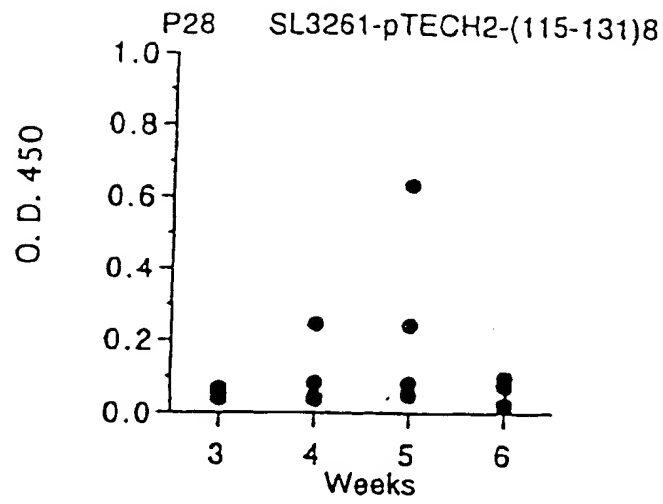


Figure 5 continued

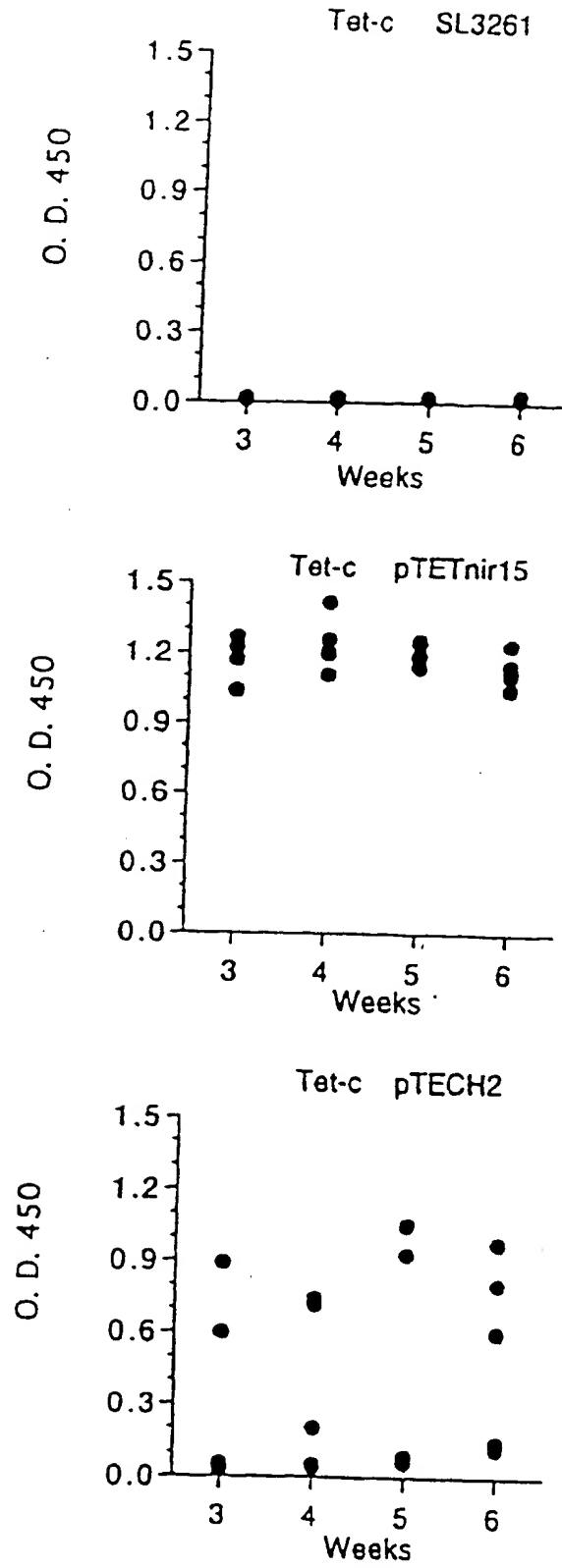


Figure 6

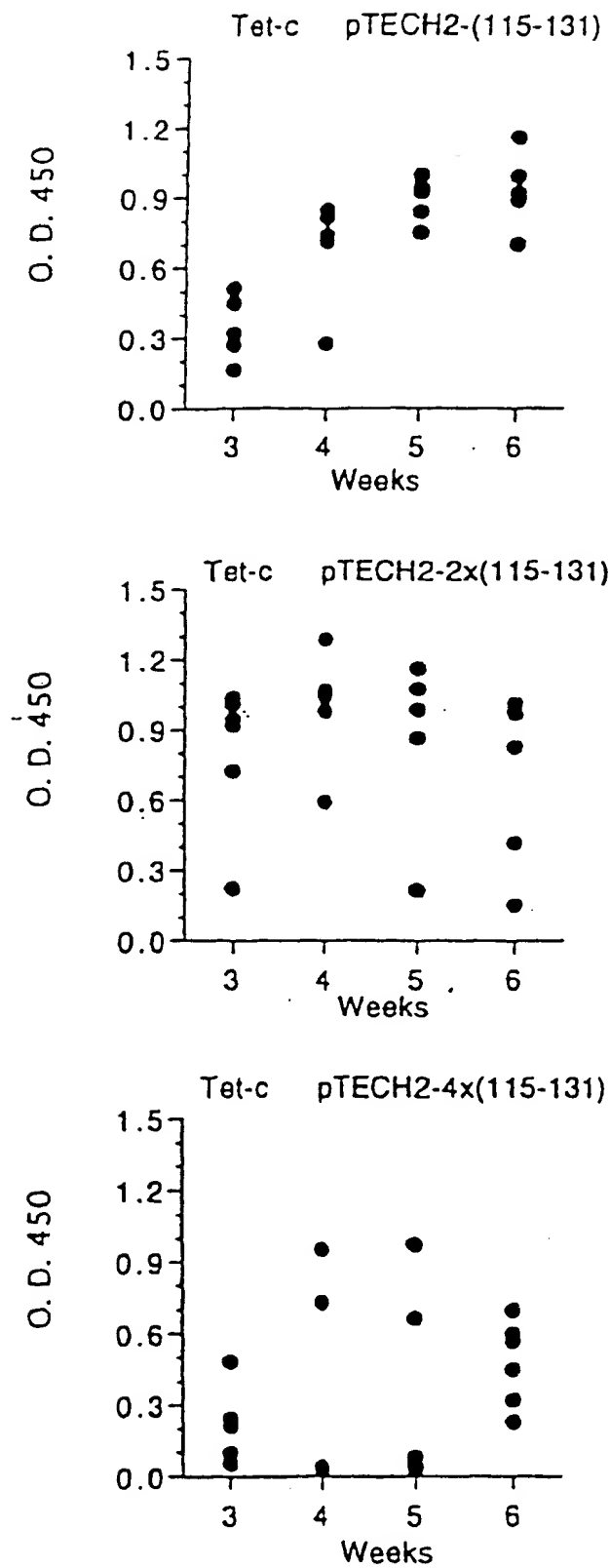


Figure 6 continued

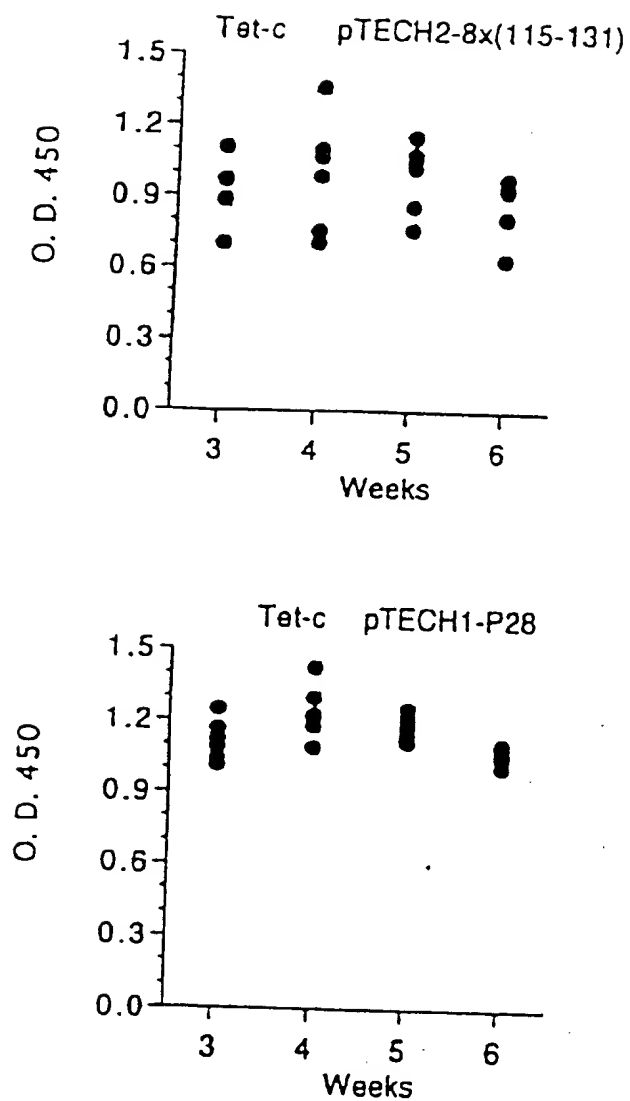


Figure 6 continued

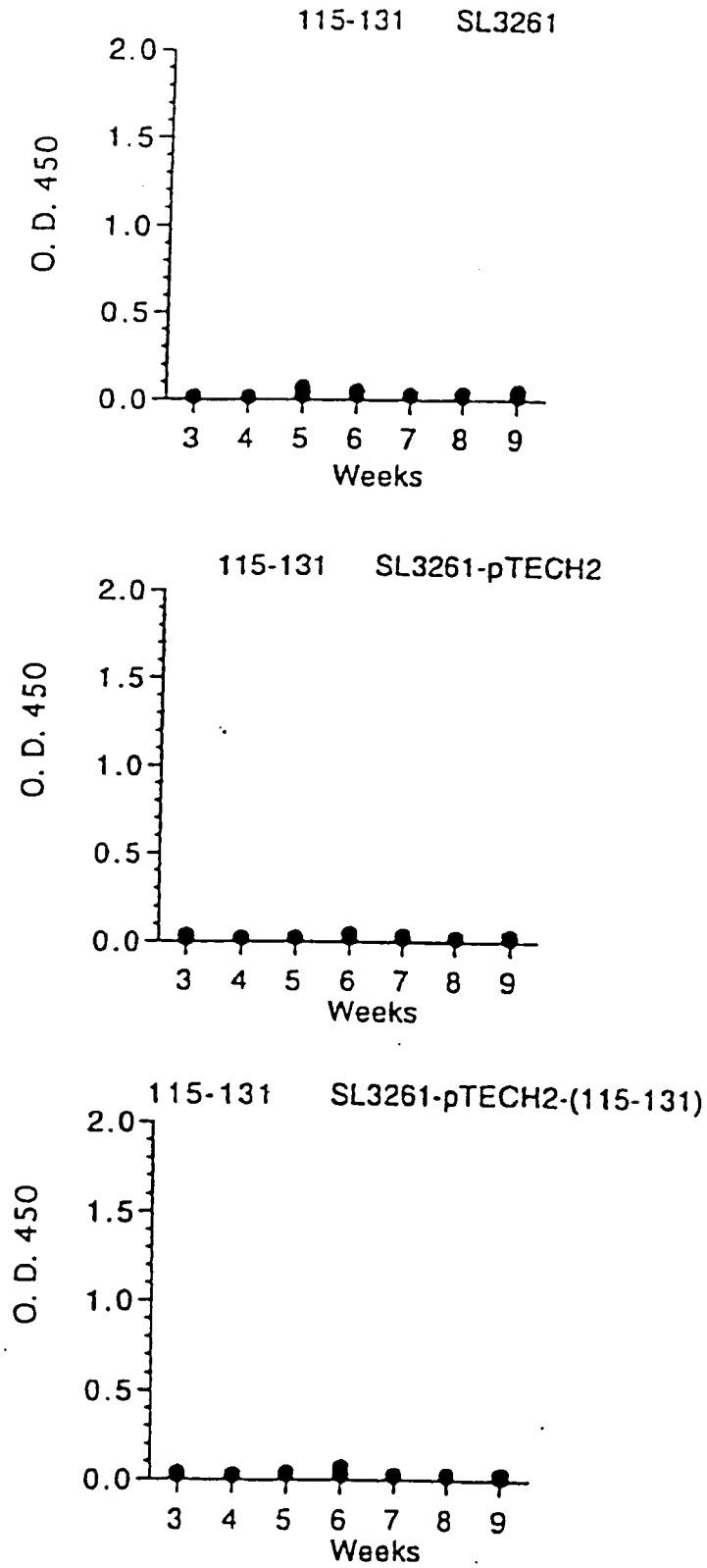


Figure 7

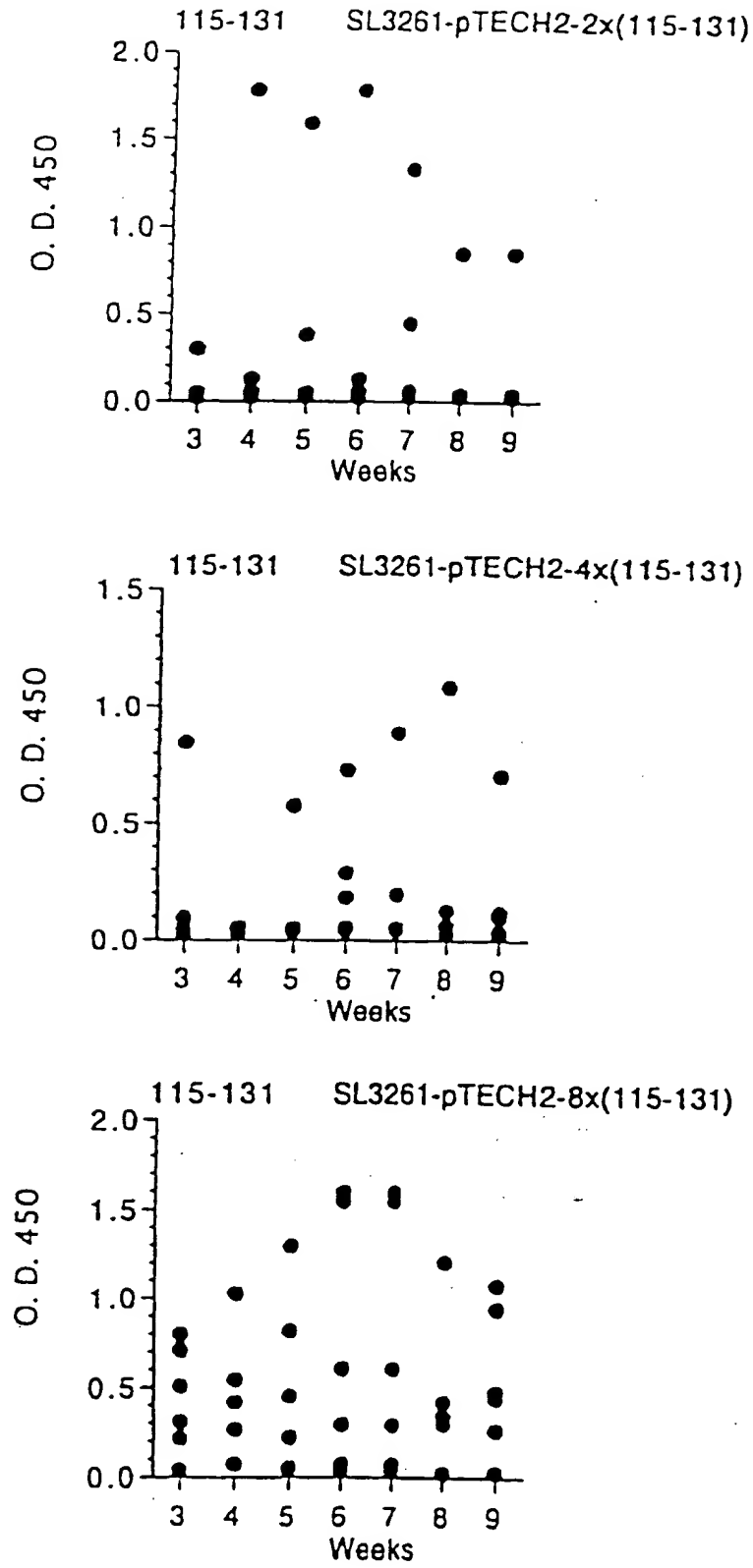


Figure 7 continued

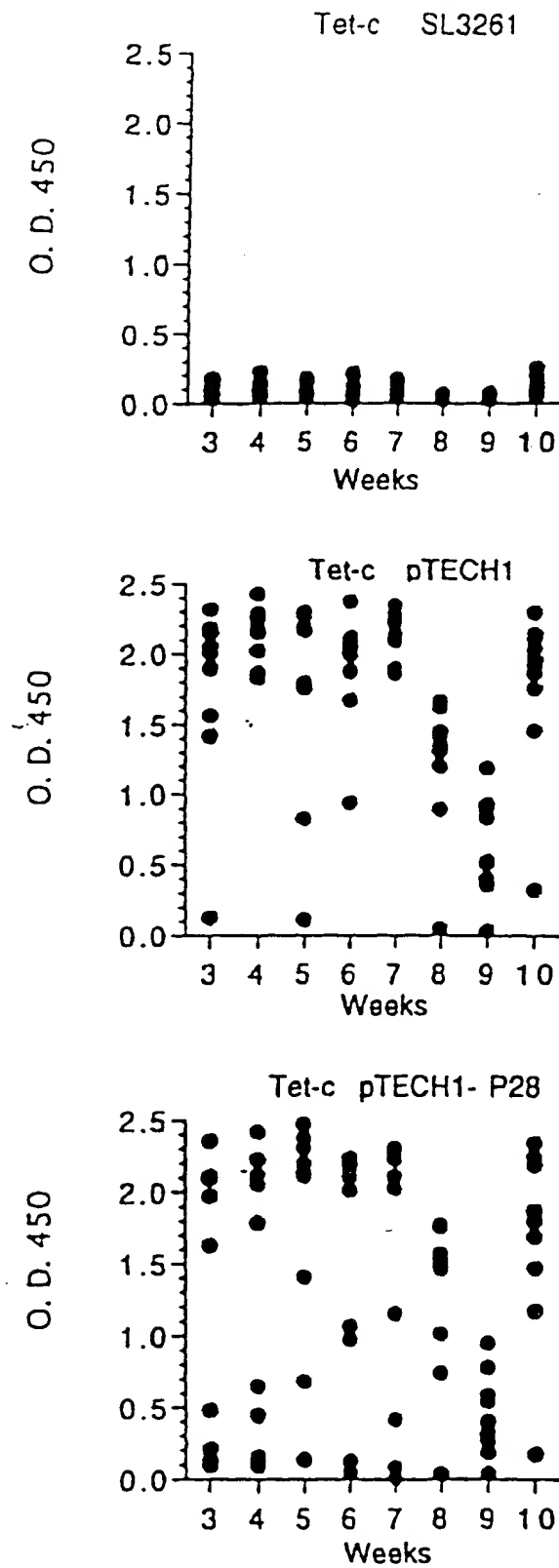


Figure 8

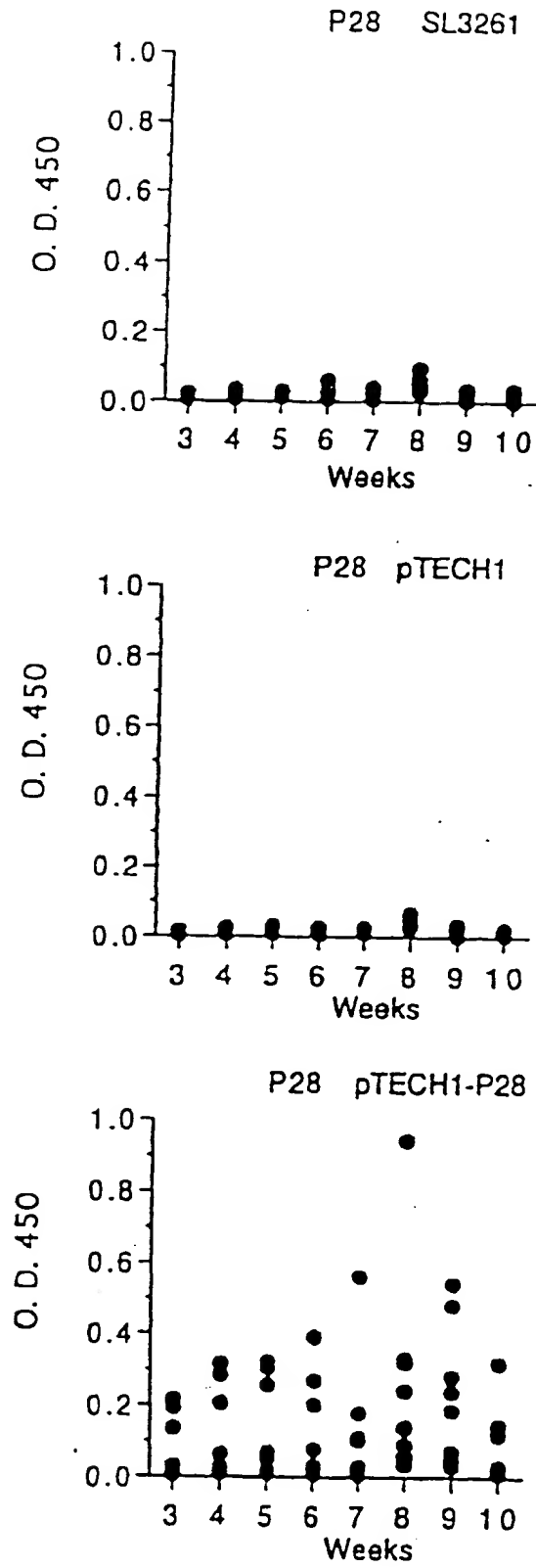


Figure 9

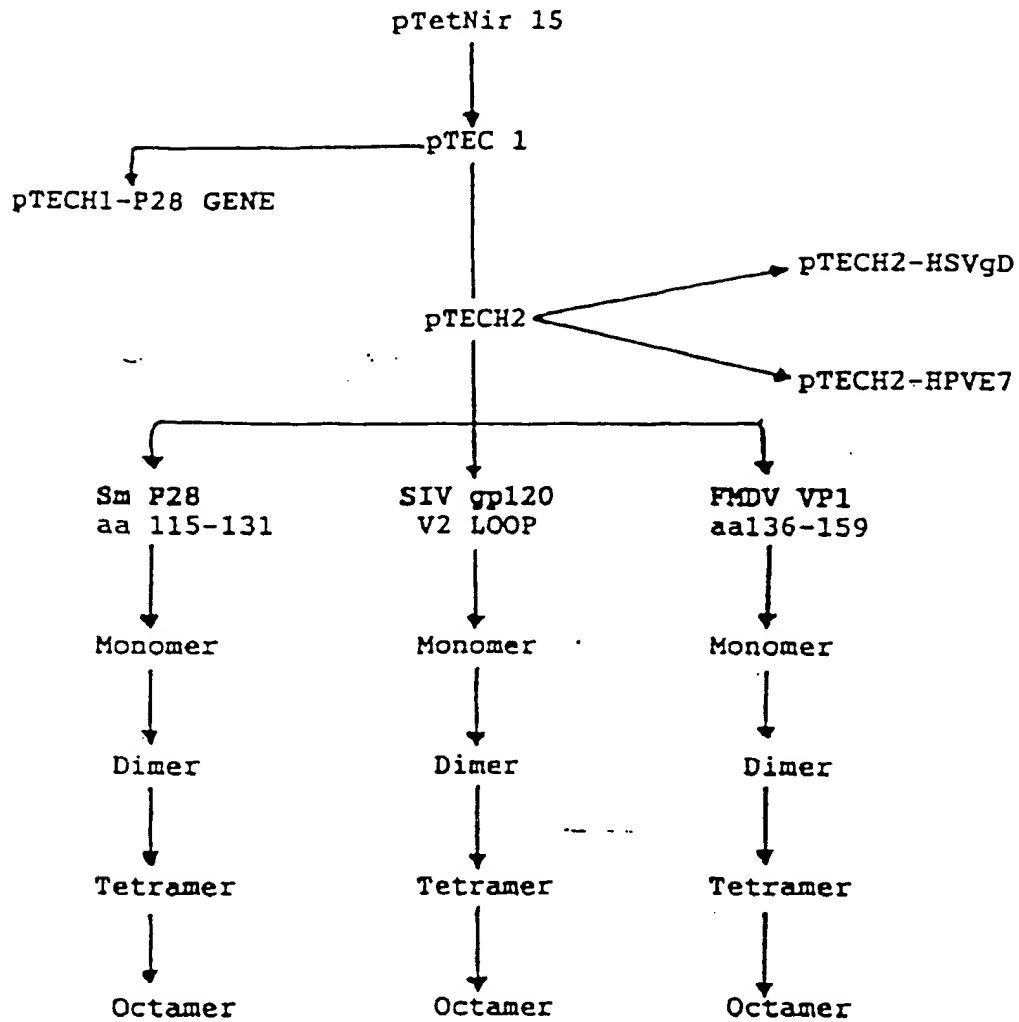
THE CONSTRUCTS

FIGURE 10

Examples of Heteromers



● = *S. mansoni* P28 epitope

▲ = SIV gp 120 V2 epitope

W = Hinge

FIGURE 11

FIGURE 12

DNA Sequence of the Vector pTECH1

(SEQ ID NO: 17)

1bp -TTGAGGTAAATTGATGTACATCAAAATGGTACCCCTTGGTGAATCGTTAAGGTAGGGGGT - 60bp

AGGGCCCAGATCTTAATCATCCACAGGAGACTTTCTGATGAAAAACCTTGATTGTGGGT

CGACAACGAGAGACATCGATGTTATCTCTGAAAAAGTCTACCATTTCTGAACCTTGGACAT

CAACAACGATATTTCTCCGACATCTCTGGTTTCAACTCCTCTGTTATACATATCCAGA

TGCTCAATTGGTGGCGGGCATCAACGGCAAGCTATCCACCTGGTTAACAACGAATCTTC

TGAAGTTATCGTGCACAAGGCCATGGACATCGAATACAACGACATGTTCAACAACTTCAC

CGTTAGCTTCTGGCTGGCGGTTCGGAAAGTTTCTGCTTCCACCTGGAACGTAACGGCAC

TAACGAGTACTCCATCTATAGCTCTATGAAGAACTCTCCCTGTCCATCGGCTCTGGTTG

GTCTGTTTCCCTGAAGGTTACAACCTGATCTGGACTCTGAAGAATCCGCGGGCGAAGT

TGGTCAGATCACTTCCGGACCTGCGGACAAGTTCAACGGGTACCTGGCTAACAAATG

GGTTTCTATCAGTATCACTAACGATGGTCTGTCTCTGCTAACCTGTACATCAACGGGT

TCTGATGGGCTCCGCTGAATCACTGGTCTGGGGCTATCCGTGAGGACAACAACATCAC

TCTTAAGCTGGACCGTTGCAACAAGACAACCGTAGGTATCCATCGACAAGTTCGGTAT

CTTCTGCAAGCACTGAACCCGAAGAGATCGAAAACTGTATACCAGCTACCTGTCTAT

CACCTTCTGGGTGACTTCTGGGGTAACCGGTGGGTACGACACCGAATATTACTGTAT

CCGGTAGCTTCTAGCTCTAAGACGTTGAGCTGAAAAACATCACTGACTACATGTACCT

GACCAACGGCGGCTCTACTAAGGTAAACTGAACATCTACTACCGACGTCTGTACAA

CGGCTGAATTCATCATCAACGGCTACACTCCGAACAACGAATCGATCTTTCTGTTAA

ATCTGGTGACTTCATCAAACTGTACGTTTCTTACAAACAACGAACACATCGTTGGTTA

CCGGAAGACGGTAACGCTTTCACAACTGGACAGAAATTCGGGTGTGGTTACAAAGC

TCCGGTATCCCGCTGTACAAAAAATGGAAGCTGTAAACTGGGTGACCTGAAACCTA

CTCTGTTTCAAGTGAACCTGTACGACGACAAAAAGCTTCTCTGGGTCTGGTTGGTACCA

CAAGGTCAGATCGTTAAGCAACCGAACCGTGACATCCTGATCGCTACTAATGGTACTT

CAACCACTGAAGACAAAACTCTGGGTTGCGACTGGTACTTCTGTTCCGACCGATGAAGG

TTGGACCAACGACGGGCGGGGCTCTAGAACTACTAGTTAAGGATTCGGTAGCCCGCC

pTECH1 DNA Sequence continued

TAATGAGCGGGCTTTTTTTTCTCGGGCAGCGTTGGGTCTCGCCACGGGTGCGCATGATC
 GTGCTCCTGTGTTGAGGACCCGGCTAGGCTGGCGGGGTTCCTTACTGGTTAGCAGAAT
 GAATCACCGATACGCGAGOGAACGTGAAGCGACTGCTGCTGCAAAAACGTCTGCGACCTGA
 GCAACAACATGAATGGTCTTCGGTTTCCGTGTTTCGTAAAGTCTTGAAACGCGGAAGTCA
 GCGCTCTTCGGCTTCTCGCTCACTGACTCGCTCGCTCGGTGTTTCGGCTGCGGCGAGC
 GGTATCAGCTCACTCAAAGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGG
 AAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCGCGTTGCT
 GCGCTTTTTCCATAGGCTCCGCCCCCCCTGACGAGCATCAGAAAAATCGACGCTCAAGTCA
 GAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGCGTTTCCCCCTGGAAGCTCCCT
 CGTGGGCTCTCCGTTCOGACCCCTGCGCTTACCGGATACCTGTCCGCTTTCTCCCTTC
 GGAAGCGTGGCGCTTTCTCAATGCTCAGCGTGTAGGTATCTCAGTTCGGTGTAGGTGCT
 TCGCTCCAAGCTGGGCTGTGTGCAGGAACCCCCCGTTACGCCGACCGCTGCGCCTTATC
 CGGTACTATCGTCTTGAGTCCAACCGGTAAGACAGACTTATGCCACTGGCAGCAGC
 CACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTG
 GTGGCCTAACTACGGCTACACTAGAAGGACAGTATTGGTATCTCGGCTCTGCTGAAGCC
 AGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAACAAACCACCGCTGGTAG
 CGGTGGTTTTTTTGTGTTGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGA
 TCCTTTGATCTTTTCTAAGGGGTCTGACGCTCAGTGGAAACGAAAACCTCAAGTTAAGGGAT
 TTTGGTCATGAGATTATCAAAAAGGATCTTCACCTAGATCTTTTAAATTAAAAATGAAG
 TTTTAAATCAATCTAAAGTATATATGAGTAAACTTGGTCTGACAGTTACCAATGCTTAAT
 CAGTGAGGCACTATCTCAGCGATCTGTCTATTTGTTTCATCCATAGTTGCCCTGACTCCC
 CGTGTGTAGATAACTACGATACGGGAGGGCTTACCATCTGGCCCCAGTGCTGCAATGAT
 ACCCGAGACCCACGCTCACCGGCTCCAGATTTATCAGCAATAAACCCAGCCAGCCGGAAG
 GGCCGAGCGCAGAAGTGGTCTGCAACTTTATCCGCTCCATCCAGTCTATTAAATTGTTG

pTECH1 DNA Sequence continued

CCGGGAAGCTAGAGTAAGTAGTTCCGCCAGTTAATAGTTTGCGCAACGTTGTTGCCATTGC
TGCAGGCATCGTGGTGTCAAGCTCGTCTGTTGGTATGGCTTCATTACAGCTCCGGTTCCCA
ACGATCAAGGCGAGTTACATGATCCCCATGTTGTGCAAAAAAGCGGTTAGCTCTTTCGG
TCTTCGATCGTTGTGAGAAGTAAGTTGGCCGCGAGTGTATCACTCATGGTATGGCAGC
ACTGCATAATTCTCTTACTGTTCATGCCATCCGTAAGATGCTTTTCTGTGACTGGTGAGTA
CTCAACCAAGTCATTCTGAGAATAGTGTATGCGGCGACCGAGTTGCTCTTCCCGGCGTC
AACACGGGATAATACCGCGCCACATGCGAGAAGTTTAAAAGTGCTCATCATTGGAAAACG
TTCTTCGGGGCGAAAACCTCTCAAGGATCTTACCGCTGTGAGATCCAGTTGATGTAACC
CACTCGTGCACCCAACTGATCTTCAGCATCTTTTACTTTCACCAGCGTTTCTGGGTGAGC
AAAAACAGGAAGGCCAAAATGCCGCAAAAAGGGAATAAGGGGACACCGAAATGTTGAAT
ACTCATACTCTTCCCTTTTCAATATTTATGAAGCATTATCAGGGTATTGTCTCATGAG
CGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAGGGGTTCCGGGCACATTTCC
CCGAAAAGTGCCACCTGACGTCTAAGAAACCATTATTATCATGACATTAACCTATAAAAA
TAGGGGTATCACGAGGCCCTTTCTGTCCTCAAGAA - 3754bp

FIGURE 13

DNA Sequence of the Vector pTECH2

(SEQ ID NO: 18)

1bp - TTCAAGTTAAATTGATGTCATCAAAATGGTACCCCTTGCTGAATCGTTAAGGTAGGCGGT - 60bp

AGGGCCAGACTTAAATCACTCCACAGGAGACTTTCIGATGAAAAACCTTGATTGTGGGT

CGACAACGAAGAAGACATCGATGTATCTGAAAAAGTCTACCATTCIGAACTTGGACAT

CAACAACGATATATCTCCGACATCTCTGGTTTCACTCCTCTGTATCAGATATCCAGA

TGCTCAATTGGTGGCGGGCATCAAGGCAAGCTATCCACCTGGTTAACAACGAATCTTC

TGAAGTTATCGTGCACAAGGCGATGGACATCGAAACAAAGACATGTTCAAACTTCAC

CGTTAGCTTCTGGCTGGCGTTCCGAAAGTTCTGGTTCCCACTTGGAAACAGTACGGCAC

TAACGAGTACTCCATCATCAGGCTATGAAACAACTCCTGTCCATCGGCTCTGGTTG

GTCTGTTTCCCTGAAGGTTAAACCTGATCTGGACTCTGAAAGACTCCGCGGCGAAGT

TGCTCAGATCACTTTCGGGACCTGGCGGACAGTTCAACGGGTACCTGGCTAACAAATG

GGTTTTCATCACTATCACTAACGATCTGTCTGTCTCTGCTAACCTGTACATCAACGGGT

TCTGATGGGCTCCGCTGAATCACTGGTCTGGGCTATCTCGTGAGGACAACAACATCAC

TCTTAAGCTGGACCGTTGCAACAAACAAACCGTACGTATCCATCGACAAGTTCGGTAT

CTTCIGCAAAGCACTGAACCCGAAGAGATGAAAACTGTATACCAAGCTACCTGTCTAT

CACCTTCCTGGGTGACTTCTGGGGTAAACCGCTGGTTACGACACCGAATATTAAGTAT

CCCGGTAGCTTCTAGCTCTAAAGACTTCACTGAAAAACATCACTGACTACAGTACTT

GACCAACGCGCGTCTCTACACTAACGGTAACTGAACATCTACTACCGACTCTGTACAA

CGGCTGAAATTCATCATCAACGCTACCTCGAACAACGAATCGATTCTTTGGTTAA

ATCTGGTGACTTCATCAAACTGTACTTTCTTACAAACAACGAACACATCGTTGGTTA

CCCGAAAGACGGTAACGCTTTCACAACTGGACGAATCTCGGTGTGGTTACAACGC

TCGGGTATCCCGCTGTACAAAAAATGGAAGCTGTAACTGGGTGACCTGAAAACTTA

CTCTCTTCAAGCTGAACCTGTACGACGACAAAAAGCTTCTCTGGGTCTGTTTGGTACCA

CAACGGTCAAGTGGTTAAGACCGAACCGTACATCTGTATCCCTTCTAACTGGTACTT

CAACCACTGAAAGACAAAAATCTGGTTGGCACTGGTACTTCTGTTCGACCGATGAAGG

TTGGACCAACGACGCGCGCGGCGCTCTTGAAGATCCGACATCAACCTTACTAGTTAATG

ATCCGCTAGCCCGCTAATGAGCGGCTTTTTTTTCTCGGGCAGGTTGGGTCCCTGGCCA

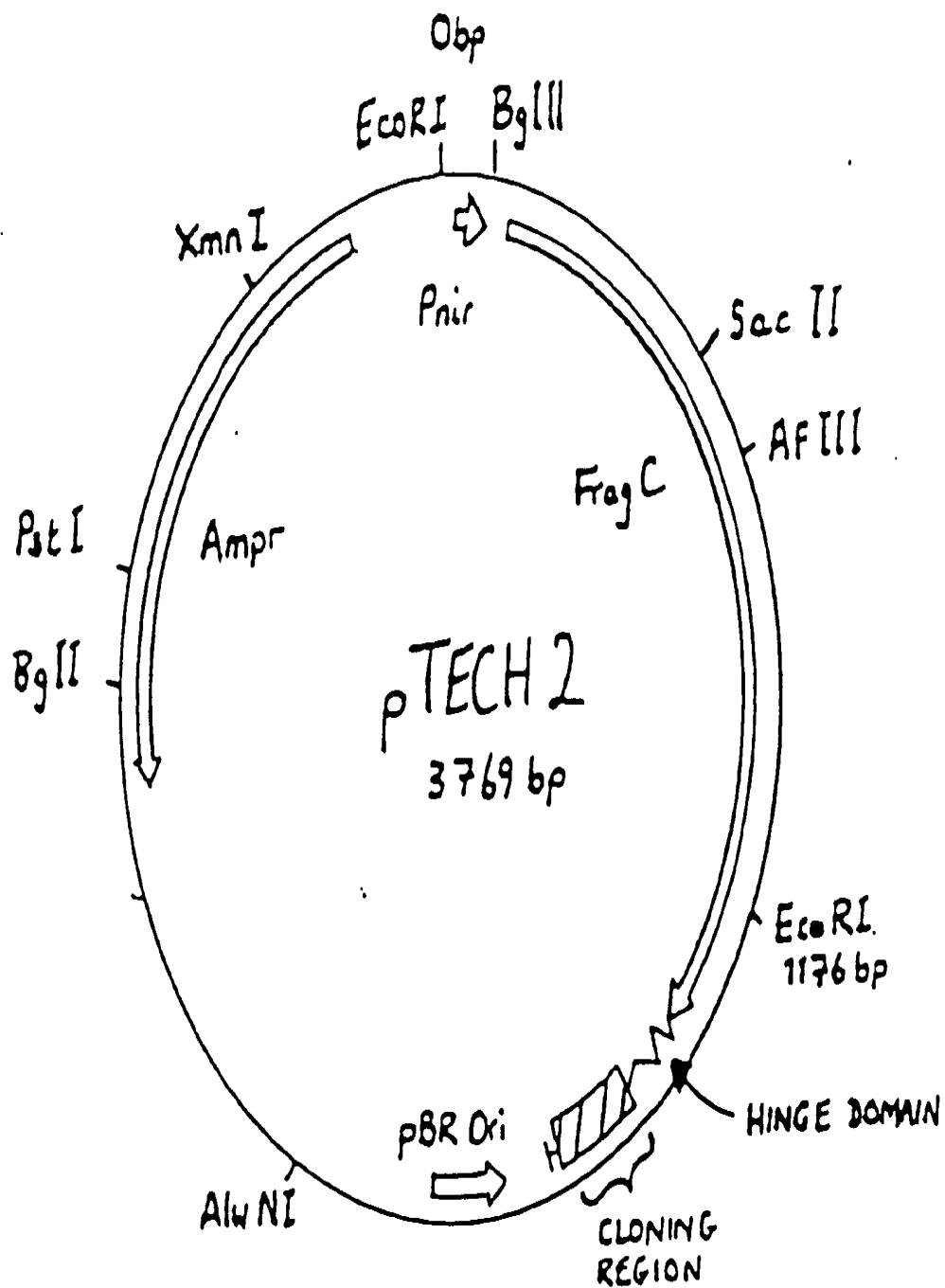
CGGTGCGCATGATCGTCTCTCTGTTTGAAGACCGGCTAGGCTGGCGGGGTTCGCTT

pTECH2 DNA Sequence continued

ACTGGTTAGCAGAATGAATCACCGATACGCGAGCGAAGTGAAGCGACTGCTGCTGCAAA
 ACGTCTGCGACCTGAGCAACAACATGAATGGTCTTCGGTTTCCGTGTTTCGTAAAGTCTG
 GAAACGCGGAAGTCAGCGCTCTTCGCTTCCTCGCTCACTGACTCGCTCGCTCGCTCGT
 TCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAAATACGGTTATCCACAGAATC
 AGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAA
 AAAGGCGCGGTTGCTGGCGTTTTTCCATAGGCTCGCCCCCTGACGAGCATCACAAAAA
 TCGACGCTCAAGTCAGAGGTGGGAAACCGACAGGACTATAAAGATACCAGGCGTTTTCC
 CCTGGAAGCTCCCTGCTGCGCTCTCTGTTCCGACCCCTGCGGCTACCGGATACCTGTC
 CGCCTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCAATGCTCAAGCTGTAGGTATCTCAG
 TTOGGTGTAGGTGCTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTACGCCGA
 CGCTGCGCCTTATCOGTTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATC
 GCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTAC
 AGAGTCTGTGAAGTGGTGGCTAACTAAGGCTACACTAGAAGGACAGTATTTGGTATCTG
 CGCTCTGCTGAAGOCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCOGGCAAACA
 AACCACCGCTGGTAGCGGTGGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAA
 AGGATCTCAAGAAGATCCTTTGATCTTTTTCTACGGGGTCTGACGCTCAGTGGAAACGAAAA
 CTCACGTTAAGGGATTTTGGTCATGAGATTATCAAAAAGGATCTTCACCTAGATCCTTTT
 AAATTAAAAATGAAGTTTTAAATCAATCTAAAGTATATATGAGTAACTTGGTCTGACAG
 TTACCAATGCTTAATCAGTGAGGCACCTATCTCAGCGATCTGTCTATTTGTTTCATCCAT
 AGTTGCCCTGACTCCCGCTCGTGTAGATAACTAOGATAOGGGAGGGCTTACCATCTGGCCC
 CAGTGCTGCAATGATACCGCGAGACCCACGCTCACCGGCTCCAGATTATCAGCAATAAA
 CCAGCCAGCGGAAGGGCGAGCGCAGAAAGTGGTCCGCAACTTTATCCGCTCCATCCA
 GTCTATTAAATGTTGTCGGGAAGCTAGAGTAAGTAGTTCCGCAAGTTAATAGTTTGCGCAA
 CGTTGTTGCCATTGCTGCAGGCATOGTGGTGTACGCTCGTCTGTTGGTATGGCTTCATT
 CAGCTCCGGTTCCCAACGATCAAGGCGAGTTACATGATCCCCATGTTGTGCAAAAAGC
 GGTEAGCTCCTTCGGTCTCCGATCGTTGTGAGAAGTAAGTTGGCCGAGTGTATCACT
 CATGGTTATGGCAGCACTGCATAATCTCTTACTGTGTCATGCCATCCGTAAGATGCTTTTC

pTECH2 DNA Sequence continued

TGTGACTGGTGAGTACTCAACCAAGTCATTCTGAGAATAGTGTATGCGGCGACCGAGTTG
 CTCCTGCGCGGGGTCAACAAGGATAATACCGGCGCACATAGCAGAACTTTAAAGTGCT
 CATCATTTGGAACCGTTCTTCGGGGCGAAACTCTCAAGGATCTTACCGCTGTTGAGATC
 CAGTTGATGTAAACCACTGCTGCACCCAACTGATCTTCAGCATCTTTTACTTTCAACCAG
 CGTTTCTGGGTGAGCAAAACAGGAAGGCAAAATGCGCAAAAAGGGAATAAGGGCGAC
 ACGGAATGTTGAATACTCATACTCTTCCTTTTCAATATTATTGAAGCATTTATCAGGG
 TTATTTGCTCTATGAGCGGATACATATTTGAATGTATTTAGAAAAATAACAAATAGGGGT
 TCGCGGCACATTTCCCGAAAAGTGCCACCTGACGTCCTAAGAAACCATTTATCATGAC
 ATTAACCTATAAAAAATAGGCGTATCAGGAGGCCCTTTTGTCTTCAAGAA





European Patent
Office

EUROPEAN SEARCH REPORT

Application Number
EP 98 10 4783

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Place of search THE HAGUE		Date of completion of the search 9 June 1998	Examiner Hornig, H
CATEGORY OF CITED DOCUMENTS X: particularly relevant if taken alone Y: particularly relevant if combined with another document of the same category A: technological background O: non-written disclosure P: intermediate document		T: theory or principle underlying the invention E: earlier patent document, but published on, or after the filing date O: document cited in the application L: document cited for other reasons &: member of the same patent family, corresponding document	

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EUROPEAN SEARCH REPORT

Application Number
EP 98 10 4783

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The present search report has been drawn up for all claims				
Place of search		Date of completion of the search	Examiner	
THE HAGUE		9 June 1998	Hornig, H	
CATEGORY OF CITED DOCUMENTS X : particularly relevant if taken alone Y : particularly relevant if combined with another document of the same category A : technological background O : non-written disclosure P : intermediate document T : theory or principle underlying the invention E : earlier patent document, but published on, or after the filing date D : document cited in the application L : document cited for other reasons & : member of the same patent family, corresponding document				

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Application Number
EP 98 10 4783

DOCUMENTS CONSIDERED TO BE RELEVANT			
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The present search report has been drawn up for all claims			
Place of search THE HAGUE		Date of completion of the search 9 June 1998	Examiner Hornig, H
<p>CATEGORY OF CITED DOCUMENTS</p> <p>X : particularly relevant if taken alone Y : particularly relevant if combined with another document of the same category A : technological background O : non-written disclosure P : intermediate document</p> <p>T : theory or principle underlying the invention E : earlier patent document, but published on, or after the filing date D : document cited in the application L : document cited for other reasons & : member of the same patent family, corresponding document</p>			

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